

STIC-Biotech/ChemLib

121108

From: Chan, Christina
Sent: Tuesday, May 04, 2004 1:22 PM
To: Wilder, Cynthia; STIC-Biotech/ChemLib
Subject: RE: Rush sequence search for 09/646,569

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Wilder, Cynthia
Sent: Tuesday, May 04, 2004 11:19 AM
To: Chan, Christina
Subject: Rush sequence search for 09/646,569

Ms. Chan,

I am requesting a rush sequence search for 09/646569 because this case needs prompt attention. Please forward your approval to STIC.

Please provide a standard search and for interference of SEQ ID NO: 60.

Thank you

Cynthia B. Wilder, Ph.D.
United States Patent and TradeMark Office
Carlyle Remson 2A35
Mailbox: 2C18
571/272-0791

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: 1
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 13:51:38 ; Search time 5401 Seconds

(without alignments)
11561.159 Million cell updates/sec

Title: US-09-646-569a-60

Perfect score: 2091

Sequence: 1 aagagacagacttaactc.....ggagagagggggggagagc 2091

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estcin:*
4: em_estcma:*
5: em_estov:*
6: em_estdpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_esthum:*
18: em_estinv:*
19: em_estpin:*
20: em_estvrt:*
21: em_estfun:*
22: em_estmam:*
23: em_estmus:*
24: em_estpro:*
25: em_estpod:*
26: em_estphg:*
27: em_estvrt:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1919.8	91.8	2043	11	AF172821 Homo sapi
2	1909.4	91.3	2317	11	AF173551 Homo sapi
3	1889.6	90.4	1908	11	AF176919 Homo sapi
4	1878.6	89.8	1909	11	AF113212 Homo sapi

5	927	44.3	1019	13	BX354115	BX354115
6	887.2	42.4	1201	9	AL523087	AL523087
7	864.4	41.3	893	13	BQ940216	BQ940216
8	838	40.1	1047	13	BX354114	BX354114
9	831.6	39.8	956	13	BH151512	BH151512
10	801	38.3	921	13	BQ881763	BQ881763
11	796	38.1	880	12	B1752648	B1752648
12	783.4	37.5	1168	9	AL523086	AL523086
13	775.4	37.1	841	13	BQ720852	BQ720852
14	757.8	36.2	797	13	B0568349	B0568349
15	732.6	35.0	795	12	B1752817	B1752817
16	720.4	34.5	757	14	CF455226	CF455226
17	713.6	34.1	722	13	BQ940841	BQ940841
18	713.6	34.1	872	13	BQ898921	BQ898921
19	712	34.1	929	13	BQ898900	BQ898900
20	709.6	33.9	854	12	BQ428180	BQ428180
21	702.6	33.6	736	9	AV702158	AV702158
22	690.2	33.0	804	12	B1752647	B1752647
23	674.4	32.3	728	14	CD250756	CD250756
24	670	32.0	769	14	CD511615	CD511615
25	663	31.7	764	14	CD298779	CD298779
26	661	31.6	661	14	CD677889	CD677889
27	659.4	31.5	803	13	B0852225	B0852225
28	635	30.4	635	14	CD677590	CD677590
29	623.8	29.8	809	14	CB309328	CB309328
30	619	29.6	619	14	CD679506	CD679506
31	616	29.5	627	14	CD676866	CD676866
32	611.6	29.2	793	13	BQ441408	BQ441408
33	610.2	29.2	669	12	BM729000	BM729000
34	607.8	29.1	612	9	AL693723	AL693723
35	607.4	29.0	616	12	BG35597	BG35597
36	604	28.9	604	12	BM998093	BM998093
37	604	28.9	795	14	CB962278	CB962278
38	597.8	28.6	686	12	BG928675	BG928675
39	597.4	28.6	712	9	AV727906	AV727906
40	596.2	28.5	989	10	BE887170	BE887170
41	594.6	28.4	623	12	BQ002622	BQ002622
42	591.4	28.3	594	9	AA928698	AA928698
43	590.4	28.2	593	14	CB266994	CB266994
44	590	28.2	673	10	AW964463	AW964463
45	588.6	28.1	711	14	CB962541	CB962541

ALIGNMENTS

RESULT 1
AF172821 2043 bp mRNA linear HTC 01-AUG-2003
LOCUS Homo sapiens MSTP092 (MST092) mRNA, complete cds.
DEFINITION AF172821
ACCESSION AF172821
VERSION AF172821.1 GI:33337985
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2043)
Liu, B., Song, L., Sheng, H., Qin, B.M., Liu, Y.Q., Zhao, B., Wang, X.Y.,
Zhang, Q., Ji, X.Y., Liu, B.H., Lu, H., Xu, H.S., Chen, J.Z., Cai, M.Q.,
Zheng, W.Y., Teng, C.Y., Liu, Q., Yu, L.T., Lin, J., Gong, J.,
Zhang, A.M., Gao, R.L. and Hu, R.T.
Submitted (28-JUL-1999) Molecular Medicine Center for
Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167,
Bei Li Shi Lu, Beijing 100037, P.R. China
Location/Qualifiers
1..2043
/organism="Homo sapiens"
/mol_type="mRNA"
/cd_xref="taxon:9606"
/tissue_type="aorta"
1..2043
gene

OY		198	CCACAAATCAGCACTATTGTAATAATATATATCATATATACAGCAAAAAAAGAGA	2043
Dd		1981	CCACAATCACACTTTTATTATTAATATATATCTATATACAGCCAAAABAAAAA	2040
OY		2044	AGA 2046	
Dd		2041	AAA 2043	
RESULT 2				
AF173551				
LOCUS		AF173551	2317 bp	mRNA linear HTC 01-AUG-2003
DEFINITION		Homo sapiens MSTP106 mRNA, complete cds.		
ACCESSION		AF173551		
VERSION		AF173551.1	GI:33337993	
KEYWORDS		HTC.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2317) Liu,Y.Q., Sheng,H., Qin,B.M., Liu,B., Zhao,B., Wang,X.Y., Hu,J.R.T., Zhang,Q., Song,L., Liu,B.H., Lu,H., Xu,H.S., Zheng,W.Y. and Gong,J. Direct Submission Submitted (29-JUN-1999) Molecular Medicine Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing, 100037, P.R. China		
TITLE		JOURNAL		
FEATURES		source		
CDS		1..2317		
		/organism="Homo sapiens"		
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/tissue_type="aorta"		
		486..737		
		/note="MST106"		
		/codon_start=1		
		/product="MSTP106"		
		/protein_id="AA013619.1"		
		/db_xref="gi:33337994"		
		/translation="MGNNLCPLPTHTLTCTOLIKCNVLAIRIQCGELGEINYNFPP ILYKAMDFTIMCALDYSHFRNMLLIITFORVIDMKRQ"		
ORIGIN				
Query Match		91.3%; Score 1909.4; DB 11; Length 2317;		
Best Local Similarity		98.2%; Pred. No. 5,3e-303;		
Matches 2021; Conservative		0; Mismatches 11; Indels 25; Gaps 8;		
OY		1	AAGAAGACAGACTTTAACTTCGCCACGTAAATTAAGACGTATGTCAGTTATTTGTA	60
Dd		269	AAGAGACAGACTTTAACTTCGCCACGTAAATTAAGACGTATGTCAGTTATTTGTA	328
OY		61	AAGCAGTGGAATACCTTCAAGCATGGAAATATCTTCATCTCCCCG-----	111
Dd		329	AAGCAGTGGAATACCTTCAAGCATGGAAATATCTTCATCTCCCCGCACACATAC	388
OY		112	-----CGCTTTTGTTCCTTCACGGTAGAACCTTTTAAATGCAAACTTAAGTAGG	164
Dd		389	ACACACACACTTTTGTTCCTTCACGGTAGAACCTTTTAAATGCAAACTTAAGTAGG	448
OY		165	CATTTCAGTAAGTCTTGCTTCAAATCAATAAAGTCAAAATGTAAGAAACATTTGTGCC	224
Dd		449	CATTTCAGTAAGTCTTGCTTCAAATCAATAAAGTCAAAATGTAAGAAACATTTGTGCC	508
OY		225	TACTTCCATACCCTGCTACTCAATTTCTACTGTAATGATTTATGCTTTAAGTAGAT	284
Dd		509	TACTTCCATACCCTGCTGTAATTTCTACTGTAATGATTTATGCTTTAAGTAGAT	568
OY		285	TCAGTGCCAAGAGAACTTGTAATAATATTTATTTTTTTTATCCTTTACAA	344
Dd		569	TCAGTGCCAAGAGAACTTGTAATAATATTTATTTTTTTTATCCTTTACAA	628
OY		345	AGCCATGATTTTATTTGCTGATGTGCTCTGACACAGCCATTTCAATAGATGGA	404

Db	629	AGCCATGAGATTTTATTTGGTGAATGCTGCTGTCACAGGCCATTTGCAATGAGATGGA	688
Qy	405	GCTGTTATTTATTTTCCAAAGAGTAATAGCATGCAAAAGTTTCAATMAAAACTGGGGCCA	464
Db	689	GCTGTTATTTATTTTCCAAAGAGTAATAGCATGCAAAAGTTTCAATMAAAACTGGGGCCA	748
Qy	465	TTAAACAAATAAATTAATAAATCTATATAGCAATTCCTCTAGATTTTGGCCAAATGCTCTA	524
Db	749	TTAAACAAATAAATTAATAAATCTATATAGCAATTCCTCTAGATTTTGGCCAAATGCTCTA	808
Qy	525	TCCAATACCAAAATTTGGAATGCTTGAAAAGAGTATATTTTCACAGAAATGATTTTC	584
Db	809	TCCAATACCAAAATTTGGAATGCTTGAAAAGAGTATATTTTCACAGAAATGATTTTC	868
Qy	585	ATTATTTGAAACTGTTCCCTAGACAGGCCAATTTCCCTTTTCTCGGAGATTTAGCAAGT	644
Db	869	ATTATTTGAAACTGTTCCCTAGACAGGCCAATTTCCCTTTTCTCGGAGATTTAGCAAGT	928
Qy	645	TTAGSAGAGATATGTCATGAAAAAGAAAGGAGAAAGGAGAGAGGAGATTTAAAAA	704
Db	929	TTAGSAGAGATATGTCATGAAAAAGAAAGGAGAAAGGAGAGAGGAGATTTAAAAA	988
Qy	705	GTAAGTCTAGACCTTATGAAACGTAATCCCTTTGCTAGAAATATTTTAAAGCAAGCTCAGC	764
Db	989	GTAAGTCTAGACCTTATGAAACGTAATCCCTTTGCTAGAAATATTTTAAAGCAAGCTCAGC	1048
Qy	765	TTGGTTGAAAACGTAGTTTGTCAATCTTCCATATTTTGGACAGAGATATTTTCTGACTTGA	824
Db	1049	TTGGTTGAAAACGTAGTTTGTCAATCTTCCATATTTTGGACAGAGATATTTTCTGACTTGA	1108
Qy	825	ATGCAAGCTAGATGTMAAAATTTTATTTTATTCATCTTAAGAAACCTTGACTTGAATAAAATGAA	884
Db	1109	ATGCAAGCTAGATGTMAAAATTTTATTTTATTCATCTTAAGAAACCTTGACTTGAATAAAATGAA	1168
Qy	885	TAAATATTTGAGGGGTTTCCCTGCAATCTGAGCTTGCATGTCAGAAAGCAGAGAAATGGA	944
Db	1169	TAAATATTTGAGGGGTTTCCCTGCAATCTGAGCTTGCATGTCAGAAAGCAGAGAAATGAG -	1227
Qy	945	AAATGTAATCTCCAAACATCCAAAGCATGAAACCCAGGGGTAGGCAATTTCTATGTAGGTT	1004
Db	1228	AAATGTAATCTCCAAACATCCAAAGCATGAAACCCAGGGGTAGGCAATTTCTATGTAGG - T	1284
Qy	1005	TTGGAACATGGAAGTTTGTGTGATCTTGTTTATGTGCTGCTCAACCTGATTTAAACCTCTCT	1064
Db	1285	TTGGAACATGGAAG - TTGGTGCATCT - -GGTATGTGCTCTCAACCTGCAAT - AACCTCTCT	1340
Qy	1065	GGCTTATAGTCTCTTCATCTTATTTAGACAGACGTAATCGAACACTTGTCTTCCACAGG	1124
Db	1341	GGCTTATAGTCTCTTCATCTTATTTAGACAGACGTAATCGAACACTTGTCTTCCACAGG	1400
Qy	1125	CTCTTTAGTTAACAATTAGAGCTATGTTTGTGTAAACAACCTTTACCAAAATAGG	1184
Db	1401	CTCTTTAGTTAACAATTAGAGCTATGTTTGTGTAAACAACCTTTTACCAAAATAGG	1460
Qy	1185	TTCTGAGGCAACAGAGCAATGACTATTTTAAAGAAAGGCTTTCCAGCATCACTTAAC	1244
Db	1461	TTCTGAGGCAACAGAGCAATGACTATTTTAAAGAAAGGCTTTCCAGCATCACTTAAC	1520
Qy	1245	ATCCCAAAACGTAAAAAGATCAACCTTCCCACTGAGAAAAGACTCCMGGGCTTGAATGGA	1304
Db	1521	ATCCCAAAACGTAAAAAGATCAACCTTCCCACTGAGAAAAGACTCCMGGGCTTGAATGGA	1580
Qy	1305	AACTTACAGCAGAGTCAACAGGCCACAGGCCAACACAGCAACAACAAATTGGAA	1364
Db	1581	AACTTACAGCAGAGTCAACAGGCCACAGGCCAACACAGCAACAACAAATTGGAA	1640
Qy	1365	TATTAATTCACACTCAAGTTTATTAATTAATCACTTAATTTTCTAGTGAAGAACTAC	1424
Db	1641	TATTAATTCACACTCAAGTTTATTAATTAATCACTTAATTTTCTAGTGAAGAACTAC	1700
Qy	1425	AAATCAGGCTTCTCAACATTTATATAGATTTAAGAGCTCTTGCAAGTATCTGTCT	1484

Db	1701	AAATCAGCCCTTTCACACTTATTATPACAGTATTAAAGCCCTTCGAAAGTACTGTCT	1765
QY	1485	CTCACCTGAGTATTTTTTTCCTCCCACTTCGCCCTGTCTCCCTCTCTTCC	1544
Db	1761	CTCACCTGAGTATTTTTTTCCTCCCACTTCGCCCTGTCTCCCTCTCTTCC	1820
QY	1545	TTTCAGAGAGAAATATTAAACATATTGGGTCCAACTTCATATGTAATTAATAC	1604
Db	1821	TTTCAGAGAGAAATATTAAACATATTGGGTCCAACTTCATATGTAATTAATAC	1880
QY	1605	ATTAAAGCATTTAACTTCCTTTCTAGAAAATGCAGGCTAAAGCATAGACAAACAA	1664
Db	1881	ATTAAAGCATTTAACTTCCTTTCTAGAAAATGCAGGCTAAAGCATAGGAAAAACAA	1940
QY	1665	AGAGAAATGCTGAGAAATTTTGCACCTGGAGCAAGCATCTGAATTAATATTGGCAAA	1724
Db	1941	AGAGAAATGCTGAGAAATTTTGCACCTGGAGCAAGCAATCTGAATTAATATTGGCAAA	2000
QY	1725	GTTCTTTTATGTCAATAGTGTGTCAGATTTGAAGAGACTATTTTTTTTATGTGCA	1784
Db	2001	GTTCTTTTATGTCAATAGTGTGTCAGATTTGAAGAGACTA-TTTTTTTTATGTGCA	2059
QY	1785	CTAGCACTCATCTTGGAGAGCACAGCCAGAGATGATGATGAAGTGAAGTTTATA	1844
Db	2060	CTAGCACTCATCTTGGAGAGCACAGCCAGAGATGATGATGAAGTGAAGTTTATA	2119
QY	1845	AATCATTTGTAAAGATTTATGCCATATATTTTAATCAGAAATAATGTGTTATCTT	1904
Db	2120	AATCATTTGTAAAGATTTATGCCATATATTTTAATCAGAAATAATGTGTTATCTT	2179
QY	1905	TAGAATTTGTATCAATCTTATATGTACTATGTACTCATGCTCTTGATTAATTAAGC	1964
Db	2180	TAGAATTTGTATCAATCTTATATGTACTATGTACTCATGCTCTTGATTAATTAAGC	2239
QY	1965	ACCAAAATATGTATCTGTAAACCAATCACACATATATATTAATATATCTATATAAC	2024
Db	2240	ACCAAAATATGTATCTGTAAACCAATCACACATATATATTAATATATCTATATAAC	2299
QY	2025	AGCCAAAAAATAAAAA 2041	
Db	2300	AAAAAAAAAAAAAAAA 2316	

[illegible]

UNES	Location/Qualifiers
source	1. 1908
	/Organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
gene	/tissue_type="normal aorta"
	1. 1908

ORIGIN

```

CDS
    /gene="MSH129"
    69..320
    /gene="MSH129"
    /codon_start=1
    /product="MSH129"
    /protein_id="AA013663.1"
    /db_xref="GI:3338082"
    /translat="MGINLCPETLTITLCQIICYKNATLSRIQCGEGEINYNNFFEF
    ILYKAMDFILMCALYTSHPNRELLILIFQVIDNQKQ"

ORIGIN
    Query Match      90.4%; Score 1889.6; DB 11; Length 1908;
    Best Local Similarity 99.7%; Pred. No. 1e-299;
    Matches 1903; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

[illegible]

841 AACCAAGGGGTAGGCAATTCTATGTAGGTTTGGACATGAAAGTTGGTCATCTGGTT 900
 1034 TATGCTGGCTCAATGCTATTAACCTCTGGCTTATAGCTCTTCACTTATTTGACA 1093
 901 TATGCTGGCTCAATGCTATTAACCTCTGGCTTATAGCTCTTCACTTATTTGACA 960
 1094 AGCAGTATGACACCTTCTTGGACAGGCTCTTATGTTACATTTAGCAGCTACTG 1153
 961 AGCAGTATGACACCTTCTTGGACAGGCTCTTATGTTACATTTAGCAGCTACTG 1020
 1154 TTTGCTTTAAACACACTTTTACCAATAGGCTCTGAGGGAACGAGAGAGAGACTAT 1213
 1021 TTTGCTTTAAACACACTTTTACCAATAGGCTCTGAGGGAACGAGAGAGAGACTAT 1080
 1214 TAAAGAAAGGCTTCCGACATCACTTACATCCCAAACTAAAGATCAACTCTTCC 1273
 1081 TAAAGAAAGGCTTCCGACATCACTTACATCCCAAACTAAAGATCAACTCTTCC 1140
 1274 AACTGAGAAAGACTCTCTGGCTTGAATGGAATCTTACAGAGAGAGTCAAGGCCAC 1333
 1141 AACTGAGAAAGACTCTCTGGCTTGAATGGAATCTTACAGAGAGAGTCAAGGCCAC 1200
 1334 CAACAACAGACACAAACAACATTTGGAATATTATTTCACTCACTGTTTATATATA 1393
 1201 CAACAACAGACACAAACAACATTTGGAATATTATTTCACTCACTGTTTATATATA 1260
 1394 CATCTTATTTATTTCTAGTAGAGAACTACAAATCAGCTCTTCAACTTTATATACAG 1453
 1261 CATCTTATTTATTTCTAGTAGAGAACTACAAATCAGCTCTTCAACTTTATATACAG 1320
 1454 TTTATATAGGCTCTTGAAGTAACTGTTCTCTCAGCTGAGGATTTTCTCCCTCCAC 1513
 1321 TTTATATAGGCTCTTGAAGTAACTGTTCTCTCAGCTGAGGATTTTCTCCCTCCAC 1380
 1514 CTGCGCCCTGTCCT 1573
 1381 CTGCGCCCTGTCCT 1440
 1574 GGTCCAACTTCAAT 1633
 1441 GGTCCAACTTCAAT 1500
 1634 AAATGCAAGGCTAAGGATGACAAACAAAGAGAAATGCTGAGAAATTTGCACTGGA 1693
 1501 AAATGCAAGGCTAAGGATGACAAACAAAGAGAAATGCTGAGAAATTTGCACTGGA 1560
 1694 GACAAGCAATCTGAATTAATTTTCCCAAAAGTTCTTTTATGTCATATAGTCCAGAT 1753
 1561 GACAAGCAATCTGAATTAATTTTCCCAAAAGTTCTTTTATGTCATATAGTCCAGAT 1620
 1754 TTGAAGAGAGCTATTTTATGTTGCAACTGACATCTCTTGGAGAGACACAGCC 1813
 1621 TTGAAGAGAGCTATTTTATGTTGCAACTGACATCTCTTGGAGAGAGACAGCC 1679
 1814 AGGAGATGAGTATAGTGAAGGTTTATATATATATATATATATATATATATATAT 1873
 1680 AGGAGATGAGTATAGTGAAGGTTTATATATATATATATATATATATATATATAT 1739
 1874 TTTTAAATTCAGAAATATGTTGTTATCTTATGAAATTTGATTCATATCTTATATGAC 1933
 1740 TTTTAAATTCAGAAATATGTTGTTATCTTATGAAATTTGATTCATATCTTATATGAC 1799
 1934 TATGAGACTCATGCTTCTGAGTAAATTAAGCACCAATATGATCTGTAACCAATATAC 1993
 1800 TATGAGACTCATGCTTCTGAGTAAATTAAGCACCAATATGATCTGTAACCAATATAC 1859
 1994 AAT 2041
 1860 AAT 1907

RESULT 4
 AF113212

LOCUS AF113212 1909 bp mRNA linear HTC 12-APR-2002
 DEFINITION Homo sapiens MSTP032 mRNA, complete cds.
 ACCESSION AF113212
 VERSION AF113212.1 GI:11640571
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1909)
 AUTHORS Liu, B., Liu, Y. Q., Wang, X. Y., Zhao, B., Sheng, H., Zhao, X. W., Liu, S.,
 Xu, Y. Y., Ye, J., Song, L., Gao, Y., Zhang, C. L., Zhang, J., Wei, Y. J.,
 Qiang, H. Q., Zhao, Y., Liu, L. S., Ding, J. F., Gao, R. L., Wu, Q. Y.,
 Qiang, B. Q., Yuan, J. G., Liew, C. C., Zhao, M. S. and Hui, R. T.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
 Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
 Beijing 100037, P. R. China
 FEATURES
 Source location/Qualifiers
 1..1909
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cissue_type="aorta"
 69..320
 /codon_start=1
 /product="MSTP032"
 /protein_id="M33283.1"
 /db_xref="GI:11640572"
 /translation="MVGNIICPTLHCTOLYCKMYALSRIOCGEIGELNYRFF
 ILYKMPFIWLMCALYSHFNMELLIIIFRVIDMKFO"
 ORIGIN
 Query Match 89.8%; Score 1878.6; DB 11; Length 1909;
 Best Local Similarity 99.7%; Pred No. 6.4e-298;
 Matches 1903; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 134 GACACCTTTTAAATGACAGAACTAATGAGCAATTCAGTAATCTTGTCTTCAATCAT 193
 1 GACACCTTTTAAATGACAGAACTAATGAGCAATTCAGTAATCTTGTCTTCAATCAT 60
 194 AAAGTCAATGATGGAAGAACTTTTGGCCCTACTCTCCATCCCGCTACTCAATTC 253
 61 AAAGTCAATGATGGAAGAACTTTTGGCCCTACTCTCCATCCCGCTACTCAATTC 120
 254 TCTACTGATGATTAATGCTTTAGTAGAATTCAGTCCAGAGAACTTGTGAAATTA 313
 121 TCTACTGATGATTAATGCTTTAGTAGAATTCAGTCCAGAGAACTTGTGAAATTA 180
 314 ATTATTTTAAATTTTATTTTATCTTCAAGCAATGATTTTATGTTGATGATG 373
 181 ATTATTTTAAATTTTATTTTATCTTCAAGCAATGATTTTATGTTGATGATG 240
 374 CTCTGACACAGCCATTTCAATAGAGATGAGCTGTTAATTTTCCAAAGATATAG 433
 241 CTCTGACACAGCCATTTCAATAGAGATGAGCTGTTAATTTTCCAAAGATATAG 300
 434 ACATGCAAAAGTTTCAATATAAACTGGCCATTAACAAATTAATTAATTAATTAAC 493
 301 ACATGCAAAAGTTTCAATATAAACTGGCCATTAACAAATTAATTAATTAATTAAC 360
 494 ATTCCCTCTAGGTTTTCGCAAACTGCTATCAATTAACAAATTTAGAAATGTTGAA 553
 361 ATTCCCTCTAGGTTTTCGCAAACTGCTATCAATTAACAAATTTAGAAATGTTGAA 420
 554 AACCTATATATTTCAAGAAATGATTTTCAATTAATTAATTAATTAATTAATTAAC 613
 421 AACCTATATATTTCAAGAAATGATTTTCAATTAATTAATTAATTAATTAATTAAC 480
 614 ATTTCCTTTTCCGGGAGTTTACAGATTTAGAGAGAAATGATCATGAAAGAAAG 673
 481 ATTTCCTTTTCCGGGAGTTTACAGATTTAGAGAGAAATGATCATGAAAGAAAG 540

QY	674	GAAGAAAGGGGAGAGAGGAAAGAGGTTAAAGAAAGTACGACAACCTAAGAAAGTAATCC	733
Db	541	GAAGAAAGGGGAGAGAGGAAAGAGTTAAAGAAAGTAAGTCTCAACCTAAGAAAGTAATCC	600
QY	734	CTTGTGCTAGAAATATTTTAAGAGCAGCTCAGCTTGTTGAAACTGAGTTTGTGATCTTCC	793
Db	601	CTTGTGCTAGAAATATTTTAAGAGCAGCTCAGCTTGTTGAAACTGAGTTTGTGATCTTCC	660
QY	794	ATATTTCAGAGAAAGTAATTTTCTGACTTGCATAGCAGCTGATGTAATTTATATTATP	853
Db	661	ATATTTCAGAGAAAGTAATTTTCTGACTTGCATAGCAGCTGATGTAATTTATTTAT	720
QY	854	CATCCCTAGAAAGCCTTACTAGAAAAATGAAATATTAAGGGTTTCTGTCCATATCT	913
Db	721	CATCTAGAAAGCCTTACTAGAAAAATGAAATATTAATGAGGGTTTCTGTCCATATCT	780
QY	914	GGCTTGCAATGTGCCAGAAAGCAGAAATAGAAAAATGTAATCTCCACATCCAGCAATCA	973
Db	781	GGCTTGCAATGTGCCAGAAAGCAGAAATAGAAAAATGTAATCTCCAAATCAACGATCA	840
QY	974	AAACCAAGGGGTAGGCAATCTATGTAGTTTGACATAGAATGGTGGTCACTTGTT	1033
Db	841	AAACCAAGGGGTAGGCAATCTATGTAGTTTGACATAGAATGGTGGTCACTTGTT	900
QY	1034	TATGTGGCTCAACTGCTATTTAAACTCTCTGCTTAATGATCTGTTATTTATTAACA	1093
Db	901	TATGTGGCTCAACTGCTATTTAAACTCTCTGCTTAATGATCTGTTATTTATTAACA	960
QY	1094	AGCAGCATGGAACACTGCTTGCGACAAGGCTCTTAGTTAACATTTAGCAGTACTG	1153
Db	961	AGCAGCATGGAACACTGCTTGCGACAAGGCTCTTAGTTAACATTTAGCAGTACTG	1020
QY	1154	TTTGTGTAAACACACTTTTACCAAAATAGGTTCTGAGGCAACGAGAGCAATGACTATT	1213
Db	1021	TTTGTGTAAACACACTTTTACCAAAATAGGTTCTGAGGCAACGAGAGCAATGACTATT	1080
QY	1214	TAAAGAAAGGCTTTCGCCAGCATCACTTACATCCCAAACTAAAGAGTCACTCTCC	1273
Db	1081	TAAAGAAAGGCTTTCGCCAGCATCACTTACATCCCAAACTAAAGAGTCACTCTCC	1140
QY	1274	AACTGAGAAAAGACTCTGCTTGTAATGAGAACTTACAGCAGAGACTCAAGGCCAGG	1333
Db	1141	AACTGAGAAAAGACTCTGCTTGTAATGAGAACTTACAGCAGAGACTCAAGGCCAGG	1200
QY	1334	CACCAACACGACACACAAACAAATTTGGAATATTATCTCACTCACTGCTTTAATATA	1393
Db	1201	CACCAACACGACACACAAACAAATTTGGAATATTATCTCACTCACTGCTTTAATATA	1260
QY	1394	CATCTT-ATTATTTTCTAGTAGAGAAACTCAATCAGCTCTTCAACATTATATACA	1452
Db	1261	CATCTTATTTATTTTCTAGTAGAGAAACTCAATCAGCTCTTCAACATTATATACA	1320
QY	1453	GTTTAATAAGCCTCTTGCAAGTACTTGTCTCTCACTGAGGTAATTTTCTCTCCCA	1512
Db	1321	GTTTAATAAGCCTCTTGCAAGTACTTGTCTCTCACTGAGGTAATTTTCTCTCCCA	1380
QY	1513	CCTTGCCCTGTCTCTCCCTTCCCTCTCTGCTCCCTTGCAAGAGAAATTTTAAATATTT	1572
Db	1381	CCTTGCCCTGTCTCTCCCTTCTCTCTCTCTCTCTTGCAAGAGAAATTTTAAATATTT	1440
QY	1573	GGGTCCAACTTCATATATGTAATTAATTAATACATTTAAAGCATTTAACTTCTCTTGA	1632
Db	1441	GGGTCCAACTTCATATATGTAATTAATTAATTAATTAATTAAGCATTTAACTTCTCTTGA	1500
QY	1633	AAATATCAAGGCTAAGGATAGCAAAACAAGAGAAATGCTGGAATTTGCACTGG	1692
Db	1501	AAATATCAAGGCTAAGGATAGCAAAACAAGAGAAATGCTGGAATTTGCACTGG	1560
QY	1693	AGACAGCAATCTGAATATAATTTGCAAAAGTTCTTTTATGTCAATAGTGCAGGA	1752
Db	1561	AGACAGCAATCTGAATATAATTTGCAAAAGTTCTTTTATGTCAATAGTGCAGGA	1620
QY	1753	TTTGAAGAGCTATTTTTTTTAATGTTGCAACTAGCAACTCATCTTGGAAGACAGAGC	1812

Db	Accession	Version	Source	Organism	Reference Authors Title Journal Comment
Db	1621	TTTGAAGAGAGCTA-TTTTTTTTTATGTTGCACTAGCAACTACCACTCATCTTGGAAACACAG			
Qy	1813	CAGAGAAATGAATAGACAGTGAAGGTTTATAATTCATTTGTAAGCATTTATCCATAT			
Db	1680	CAGAGAAATGAATAGACAGTGAAGGTTTATAATTCATTTGTAAGCATTTATCCATAT			
Qy	1873	ATTTTAATTCAGAAAAAATTTGTTTATCTTTAGATTTTGTATTCATCTTTATGTA			
Db	1740	ATTTTAATTCAGAAAAAATTTGTTTATCTTTAGATTTTGTATTCATCTTTATGTA			
Qy	1933	CTATGACATCACTGCTTCGGATTAATTAAGACCAAAATATGATCTGTAACACATCA			
Db	1800	CTATGACATCACTGCTTCGGATTAATTAAGACCAAAATATGATCTGTAACACATCA			
Qy	1993	CACATATTTATTTAAATATATATCTATATTAACGCCAAAAAATTTAAAAA			
Db	1860	CACATATTTATTTAAATATATATCTATATTAACAAAAAATTTAAAAA			
RESULT 5					
LOCUS	BX354115				
DEFINITION	BX354115 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens				
ACCESSION	BX354115				
VERSION	BX354115.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 1019)				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	BP 191 91006 EVRY cedex - France				
	Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr				
	Library was constructed by Life Technologies, a division of				
	Invitrogen. This sequence belongs to sequence cluster 379.r For				
	more information about this cluster, see				
	http://www.genoscope.cns.fr/				
	cgi-bin/cluster.cgi?seq=CS0DC015AE06QPI&cluster=379.r. Contact :				
	Feng Liang Email : fliang@lifetech.com URL :				
	http://fulllength.invitrogen.com/Invitrogen Corporation 1600				
	Paradey Avenue Genoscope sequence ID : CS0DC015AE06QPI.				
FEATURES					
source	Location/Qualifiers				
	1..1019				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CS0DC015Y11"				
	/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"				
	/clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"				
	/note="1st strand cDNA was primed with a NotI-cligo (dt)				
	primer. Five prime end enriched, double-strand cDNA was				
	digested with Not I and cloned into the Not I and EcoR V				
	sites of the pCMVSPORT 6 vector. Library was normalized."				
ORIGIN					
Qy	Query Match	44.3%	Score 927;	DB 13;	Length 1019;
Db	Best Local Similarity	97.4%	Prod. No. 3.7e-142;		
	Matches 930;	Conservative 10;	Mismatches 15;	Indels 0;	Gaps 0;
Qy	1099 GTATGGAACACTTGCTTGGTGGCAAGGCTCTTATGTTAACTTTAGAGCTACTGTTGT				1158
Db	65 GGATGGAACACTTGCTTGGTGGCAAGGCTCTTATGTTAACTTTAGAGCTACTGTTGT				124
Qy	1159 GTTAAACACACTTTTACCAAAATAGTCTCTAGAGCAACGAGACGATGACATTTAAAG				1218
Db	125 GTTAAACACACTTTTACCAAAATAGTCTCTAGAGCAACGAGACGATGACATTTAAAG				184

QY 1219 AAAGGCTTCCGAGCATCACTTACACATCCCAAACTAAAAAGATCAACTCTTCCACTG 1278
 Db 185 AAAGGCTTCCGAGCATCACTTACACATCCCAAACTAAAAAGATCAACTCTTCCACTG 244
 QY 1279 AGAAAAGACTCCTGGCTTTGAATGAAAGCTTACAGCAGAGAGTCAACGGCCACGACACA 1338
 Db 245 AGAAAAGACTCCTGGCTTTGAATGAAAGCTTACAGCAGAGAGTCAACGGCCACGACACA 304
 QY 1339 ACAAAGCAACAACAACAATTTGAATTTATTTCTCAACTCAAGCTTTAATATACATCT 1398
 Db 305 ACAAAGCAACAACAACAATTTGAATTTATTTCTCAACTCAAGCTTTAATATACATCT 364
 QY 1399 TATATATTTTCTAGTAGAGAAAGCTACAAATCAGCCTCTTCAACATTTATATACAGTTTAA 1458
 Db 365 CATATTTTCTAGTAGAGAAAGCTACAAATCAGCCTCTTCAACATTTATATACAGTTTAA 424
 QY 1459 TAAAGCTCTTGCAAGTCACTTGTCTGCTCAGCTAGAGATTTTCTCCGCCACCTTGC 1518
 Db 425 TAAAGCTCTTGCAAGTCACTTGTCTGCTCAGCTAGAGATTTTCTCCGCCACCTTGC 484
 QY 1519 CCTGTCTCCTCCTCCTCTCTCTCCCTTGGCAAGAGAAATATTTAAATATTTGGGTC 1578
 Db 485 CCTGTCTCCTCCTCCTCTCTCTCCCTTGGCAAGAGAAATATTTAAATATTTGGGTC 544
 QY 1579 AACTTCAAT 1638
 Db 545 AACTTCAAT 604
 QY 1639 CACAGGCTTAAAGCAGTACAGCAAAAGCAAGAGAAATCTGAGAAATTTGGCATGAGACAA 1698
 Db 605 CACAGGCTTAAAGCAGTACAGCAAAAGCAAGAGAAATCTGAGAAATTTGGCATGAGACAA 664
 QY 1699 GCAATCTGAAAT 1758
 Db 665 GCAATCTGAAAT 724
 QY 1759 GAGAGCTATTTTCTTAAATGTTGCAATGCAACTCATCTTGGAGAGACAGCGCAGAG 1818
 Db 725 GAGAGCTATTTTCTTAAATGTTGCAATGCAACTCATCTTGGAGAGACAGCGCAGAG 784
 QY 1819 AATGAGTAGAAGTGAAGAGTTTAAATCCATTTTGAAGCATTTATCCATATATTTTA 1878
 Db 785 AATGAGTAGAAGTGAAGAGTTTAAATCCATTTTGAAGCATTTATCCATATATTTTA 844
 QY 1879 AATTCAGAAAATATGTTTATCTTTAGAAATTTTGTATCTCAATCTTATATATATATATATAT 1938
 Db 845 AATTCAGAAAATATGTTTATCTTTAGAAATTTTGTATCTCAATCTTATATATATATATATAT 904
 QY 1939 GACTCATGCTCTGATTAATTAAGACCAATATATATCTGTATACCAATATACACATA 1998
 Db 905 GACTCATGCTCTGATTAATTAAGACCAATATATATCTGTATACCAATATACACATA 964
 QY 1999 TTTATTTATATATATATCTTATATACAGCCCAAAAAAGAGAGAGAGAA 2053
 Db 965 TTTATTTATATATATATCTTATATACAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019

RESULT 6
 AL523087 1201 bp mRNA linear EST 22-MAY-2003
 LOCUS AL523087 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DC001YH21 5-PRIME, mRNA sequence.
 ACCESSION AL523087
 VERSION AL523087.2 GI:31041348
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12786580.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 379.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC001YH21&cluster=379.r. Contact :
 Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DC001YH21.

FEATURES
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC001YH21"
 /rname="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 42.4%; Score 897.2; DB 9; Length 1201;
 Best Local Similarity 97.7%; Pred. No. 1,1e-135;
 Matches 895; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1132 GTTAACAATTTAGACCTACTGTTTGTGTTAAACACACTTTTCAACCAATAGGTTCTGAG 1191
 Db 61 GATTAACAATTTAGACCTACTGTTTGTGTTAAACACACTTTTCAACCAATAGGTTCTGAG 120
 QY 1192 GCAAGAGAGCAATGATTTTAAAGAAAGCTTTCCAGCATCACTTACATATCCAA 1251
 Db 121 GCAAGAGAGCAATGATTTTAAAGAAAGCTTTCCAGCATCACTTACATATCCAA 180
 QY 1252 AACTTAAAGATCACTCTTCCACGAGAAAGATCCGAGTTTGAATGAAAGTTTAC 1311
 Db 181 AACTTAAAGATCACTCTTCCACGAGAAAGATCCGAGTTTGAATGAAAGTTTAC 240
 QY 1312 AGCAGAGAGTCAAGGCAAGCGCAACAACAACAACAATTTGAATATTTAT 1371
 Db 241 AGCAGAGAGTCAAGGCAAGCGCAACAACAACAACAATTTGAATATTTAT 300
 QY 1372 CTCACTCAGGTTTAAAT 1431
 Db 301 CTCACTCAGGTTTAAAT 360
 QY 1432 CTTCTCAACATTTAT 1491
 Db 361 CTTCTCAACATTTAT 420
 QY 1492 GAGGATTTTCTTCTCCCACTCTGCGCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1551
 Db 421 GAGGATTTTCTTCTCCCACTCTGCGCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 QY 1552 GAGGAATATTTAAACATTTTGGTCCAACTTCAATATATATATATATATATATATATATATATATAT 1611
 Db 481 GAGGAATATTTAAACATTTTGGTCCAACTTCAATATATATATATATATATATATATATATATATAT 540
 QY 1612 GCATTTAATCTCTTCTAGAAAATATGACAGGCTTAAGGATATGACAAAACAAAGAGAA 1671
 Db 541 GCATTTAATCTCTTCTAGAAAATATGACAGGCTTAAGGATATGACAAAACAAAGAGAA 600
 QY 1672 TGCTGAGAAATTTGGCAGCTGAGACAGCAATCTGAATATATATTTTGGCAAAAGTTCTTT 1731
 Db 601 TGCTGAGAAATTTGGCAGCTGAGACAGCAATCTGAATATATATTTTGGCAAAAGTTCTTT 660
 QY 1732 TTATGTCATATAGTGCAGGATTTGAAGAGGCTATTTTATATATTTGCAACTAGCA 1791

Db 661 TTATGTCANANAGTGTGAGATTTAAGAGCCATTTTATTAATGTCAGACTAGCAA 720

QY 1792 CTCATCTTCGGAAGACACAGCCAGAGAAAGAGTGAAGTGAAGGTTTAAATCCAT 1851

Db 721 CTCATCTTCGGAAGACACAGCCAGAGAAAGTGAAGTGAAGGTTTAAATCCAT 780

QY 1852 TTGTAAGCATTTATCCCATATTTTAAATTCAGAAAAATGCTTAACTTAAAT 1911

Db 781 TTGTAAGCATTTATCCCATATTTTAAATTCAGAAAAATGCTTAACTTAAAT 840

QY 1912 TTGTAATCAATCTTATATCTATGTCATGCTTCTGATTAATTAAGCAACCAAT 1971

Db 841 TTGTAATCAATCTTATATCTATGTCATGCTTCTGATTAATTAAGCAACCAAT 900

QY 1972 ATGTATCTGTACCAACATCACACATATATATTAATATATCTATTAAGCAACCA 2031

Db 901 ATGTATCTGTACCAACATCACACATATATATTAATATATCTATTAAGCAACCA 960

QY 2032 AAAAAAAAAAAGAG 2047

Db 961 AAAAAAAAAAAGAG 976

RESULT 7

BO940216 893 bp mRNA linear EST 21-AUG-2002

LOCUS BO940216

DEFINITION AGNCOURT_8654175 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:475579

ACCESSION BO940216

VERSION BO940216.1 GI:22355694

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 893)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLNL4009 row: f column: 12

High quality sequence step: 762.

Location/Qualifiers

1. 893

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:473579"

/feature_type="leucosarcoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_71"

/note="Organ: Uterus; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 2.1 kb."

ORIGIN

Query Match 41.3%; Score 864.4; DB 13; Length 893;

Best Local Similarity 98.8%; Pred. No. 6.8e-132;

Matches 880; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 703 AAGTAAGTGTGAGACCTATGACGTAATCCCTTGTCTGAATAATTTAAGACAGCTCA 762

Db 1 AAGTAAGTGTGAGACCTATGACGTAATCCCTTGTCTGAATAATTTAAGACAGCTCA 60

QY 763 GCTTGATGAACTAGTGGTTTGGCATCTCCATATTTGAGGAAGTATTTCTGACTTG 822

Db 61 GCTTGATGAACTAGTGGTTTGGCATCTCCATATTTGAGGAAGTATTTCTGACTTG 120

QY 823 CAATGACGTAGATGTAAATTTTATTTATCTATCTAGAAAAGCTTGAAGAAAATG 882

Db 121 CAATGACGTAGATGTAAATTTTATTTATCTATCTAGAAAAGCTTGAAGAAAATG 180

QY 883 AATAAATATGAGGTTTCTGTCATCTGCTGATCTGCTGATCTGCTGATCTGCTG 942

Db 181 AATAAATATGAGGTTTCTGTCATCTGCTGATCTGCTGATCTGCTGATCTGCTG 240

QY 943 GAAATGTATCTCCAAATCCAAAGCATGAAACCCAGGGGTAGGCAATTTATGAG 1002

Db 241 GAAATGTATCTCCAAATCCAAAGCATGAAACCCAGGGGTAGGCAATTTATGAG 300

QY 1003 TTTTGGACATGAAATTTGGTGGATCTTTGGTTTATGCTGGCTCACTGATTAACCTGT 1062

Db 301 TTTTGGACATGAAATTTGGTGGATCTTTGGTTTATGCTGGCTCACTGATTAACCTGT 360

QY 1063 CTGGCTTATGCTCTCTTCATTTCTATTAGACAGACGTAATGCAACTTGTGGACAA 1122

Db 361 CTGGCTTATGCTCTCTTCATTTCTATTAGACAGACGTAATGCAACTTGTGGACAA 420

QY 1123 GGCTCTTATGCTCTCTTCATTTCTATTAGACAGACGTAATGCAACTTGTGGACAA 1182

Db 421 GGCTCTTATGCTCTCTTCATTTCTATTAGACAGACGTAATGCAACTTGTGGACAA 480

QY 1183 GGTTCTGAGGCAACGAGACGTAATTTTAAAGAAAGGCTTCCAGCATCTTAC 1242

Db 481 GGTTCTGAGGCAACGAGACGTAATTTTAAAGAAAGGCTTCCAGCATCTTAC 540

QY 1243 ACATCCCAAACTTAAAGATCACTCTTCCAACTGAGAAAGACCTTGTGATG 1302

Db 541 ACATCCCAAACTTAAAGATCACTCTTCCAACTGAGAAAGACCTTGTGATG 600

QY 1303 GAACTCTACGAGAGAGTACAGGCGGCAAGCAACAGCAACCAACCAATTTGG 1362

Db 601 GAACTCTACGAGAGAGTACAGGCGGCAAGCAACAGCAACCAACCAATTTGG 660

QY 1363 AATATTAATCTCACTGCTTAAATATATATATATATATTTTCTAGTAAAGAACT 1422

Db 661 AATATTAATCTCACTGCTTAAATATATATATATATATTTTCTAGTAAAGAACT 720

QY 1423 ACAAATAGGCTCTTCAACATTTATATAGCTTAAAGCTTCAAGTACTTGT 1482

Db 721 ACAAATAGGCTCTTCAACATTTATATAGCTTAAAGCTTCAAGTACTTGT 780

QY 1483 CTCTCACTGAGGATTTTCTCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 1542

Db 781 CTCTCACTGAGGATTTTCTCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 840

QY 1543 CTTTGCAGAGGAAATTTTAACTATTTT-GGGTCCCACTTCAATTAAG 1591

Db 841 CTTTGCAGAGGAAATTTTAACTATTTTGGGTCCCACTTCAATTAAG 891

RESULT 8

EX354114/c 1047 bp mRNA linear EST 05-MAY-2003

LOCUS EX354114 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

DEFINITION cDNA clone CS00C015Y111 3-PRIME, mRNA sequence.

ACCESSION EX354114

VERSION EX354114.1 GI:30369794

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1047)

AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 379.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cgi?seq=CS0DC015AB06NP1&cluster=379.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC015AB06NP1.

FEATURES

Location/Qualifiers

1..1047
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015Y111"
/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 40.1%; Score 838; DB 13; Length 1047;
Best Local Similarity 94.4%; Pred. No. 1.3e-127;
Matches 847; Conservative 20; Mismatches 29; Indels 1; Gaps 1;
1115 TCGCACAAGCTCTTACTAGTACATTTAGCAGCTACTGTTGTGTTAAACACACTTTTC 1174
Db TCGCACAAGCTCTTACTAGTACATTTAGCAGCTACTGTTGTGTTAAACACACTTTTC 838
QY 1175 ACCAAATGGTTCTGAGGCAACGAGAGCAATGACTATTAAAGAAAGCTTTCCCGCA 1234
Db 837 ACCAAATGGTTCTGAGGCAACGAGAGCAATGACTATTAAAGAAAGCTTTCCCGCA 778
QY 1235 TCACCTACACATCCCAAACTAAAGATCACTCTTCACTGAGAAAGACTCTCGGC 1294
Db 777 TAACCTACACATCCCAAACTAAAGATCACTCTTCACTGAGAAAGACTCTCGGC 718
QY 1295 TTGTAGTGAATCTTACAGAGAGTCAAGGCGCAACGACAAACGACAAACAA 1354
Db 717 TTGTAGTGAATCTTACAGAGAGTCAAGGCGCAACGACAAACGACAAACAA 658
QY 1355 ACATTGGATATATTTCTCACTCAGCTTTAATATATCACTTATTTTCTCTGTA 1414
Db 657 ACATTGGATATATTTCTCACTCAGCTTTAATATATCACTTATTTTCTCTGTA 598
QY 1415 GAGAAACTACAAATCAGCTCTTCACTATATATACAGTTTAATTAAGCTCTTGAAGT 1474
Db 597 GAGAAACTACAAATCAGCTCTTCACTATATATACAGTTTAATTAAGCTCTTGAAGT 538
QY 1475 TACTTGTCTCTCACTCAGGATTTTCTTCCCACTTGCCTGCTTCCCTCC 1534
Db 537 CACTGTCTCTCACTCAGGATTTTCTTCCCTGCTTGCCTGCTTCCCTCC 478
QY 1535 CTCTTCTCTCTTGAAGAGAAATATTTAATATTTGGTCCCACTTCAATATGTA 1594
Db 477 CTCTTCTCTCTTGAAGAGAAATATTTAATATTTGGTCCCACTTCAATATGTA 418
QY 1595 TAATTAATACATTAAGCAATTAATCTCTTCTTGAAGAAATGACAGGCTAAGGATA 1654
Db 417 TAATTAATACATTAAGCAATTAATCTCTTCTTGAAGAAATGACAGGCTAAGGATA 358
QY 1655 GACAAACAAAGAGAAATGCTGAGAAATTTGCCACTGGAGACAGCAATCTGAATAATA 1714
Db 357 GACAAACAAAGAGAAATGCTGAGAAATTTGCCACTGGAGACAGCAATCTGAATAATA 298
QY 1715 TTGGCAAAAGTCTTTTATATGTCATATAGTTCAGAGTTTGAAGAGACTATTTTTTTT 1774
Db 297 TTGGCAAAAGTCTTTTATATGTCATATAGTTCAGAGTTTGAAGAGACTATTTTTTTT 238

QY 1775 AATGTGCACTAGCAACTCATCTTTCGGAAGACACAGCCAGAGAAATGAAGTGA 1834
Db 237 AATGTGCACTAGCAACTCATCTTTCGGAAGACACAGCCAGAGAAATGAAGTGA 178
QY 1835 AAGCTTTAATATCCATTTGTAGACATTTATCCCATATTTTAAATTAAGAAATG 1894
Db 177 AAGCTTTAATATCCATTTGTAGACATTTATCCCATATTTTAAATTAAGAAATG 118
QY 1895 TGTTTATCTTGAATTTGTATTCATATCTTATGATGATGATGATGATGATGATG 1954
Db 117 TGTTTATCTTGAATTTGTATTCATATCTTATGATGATGATGATGATGATGATG 58
QY 1955 TAATTAAGACCAAA-ATATGATCTGTATACCAATCAACATATATATTAATA 2010
Db 57 TAATTAAGACCAAAATATGATCTGTATACCAATCAACATATATTAATA 1

RESULT 9
BU151512 956 bp mRNA linear EST 03-SEP-2002
LOCUS BU151512
DEFINITION AGENCOURT_7982170 lupski_dorsal_roof_ganglion Homo sapiens cDNA
VERSION BU151512 GI:2265044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleostomi; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 (bases 1 to 956)
Nih-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Issue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL13578 row: 0 column: 05
High quality sequence start: 23
High quality sequence stop: 691.

FEATURES

source

1..956
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6186460"
/sex="male"
/issue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_roof_ganglion"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
5'-directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTGTCTTACATGCGAGCGGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 39.8%; Score 831.6; DB 13; Length 956;
Best Local Similarity 96.5%; Pred. No. 1.5e-126;
Matches 888; Conservative 0; Mismatches 14; Indels 18; Gaps 3;

QY 1 AAGAGACAGACTATTACTCCACAGCTTAATTAAAGACGTAATGTTCCATGTTTATTGTTA 60
 DB 36 AAGAGACAGACTATTACTCCACAGCTTAATTAAAGAGGTAATGTTCCATGTTTATTGTTA 95
 QY 61 AAGAGAGTGTAGTACCTTCAGACAGTGAATATCTCCATCTCCCGCG----- 111
 DB 96 AAGCAGTGTAGTACCTTCAGACAGTGAATATCTCCATCTCCCGCGACACATAC 155
 QY 112 -----CGCTTTTGTTCCTTCAGTGAACACCTTTTAAATGACAGACTAACTGAGG 164
 DB 156 ACACACACACTTTTGTTCCTTCAGTGAACACCTTTTAAATGACAGACTAACTGAGG 215
 QY 165 CATTCAGTAATCTTGTCTTCAATCAATGAATGAATGAATGAATGAATGAATGAATGAAT 224
 DB 216 CATTCAGTAATCTTGTCTTCAATCAATGAATGAATGAATGAATGAATGAATGAATGAAT 275
 QY 225 TACTCTCATACCCCGTACTCAATCTCTACTGTAATGTAATGCTTTAGTAGAAT 284
 DB 276 TACTCTCATACCCCGTACTCAATCTCTACTGTAATGTAATGCTTTAGTAGAAT 335
 QY 285 TCAGTCCCAAGAGAACTTGTGAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTA 344
 DB 336 TCAGTCCCAAGAGAACTTGTGAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTA 395
 QY 345 AGCAGTGAATTTATTTGTTGATGTCCTCTGTACACAGACATTTCAATAGATGGA 404
 DB 396 AGCAGTGAATTTATTTGTTGATGTCCTCTGTACACAGACATTTCAATAGATGGA 455
 QY 405 GCTGTTAATTTATTTTCCAAAGAGTAATAGACATGCAAAAGTTTCAATTAATACTGGGCA 464
 DB 456 GCTGTTAATTTATTTTCCAAAGAGTAATAGACATGCAAAAGTTTCAATTAATACTGGGCA 515
 QY 465 TTACCAATTAATTTAATACTTAATAGATTCCTCTAGGTTTTCGCAAACTGCTTA 524
 DB 516 TTACCAATTAATTTAATACTTAATAGATTCCTCTAGGTTTTCGCAAACTGCTTA 575
 QY 525 TCCCAATTAATTTGAGATCGTTGAAAAGCTGATTAATTTGAGAAATGATTTTC 584
 DB 576 TCCCAATTAATTTGAGATCGTTGAAAAGCTGATTAATTTGAGAAATGATTTTC 635
 QY 585 ATTATTTGAATCTTCTCCCTAGCAGGCAATTTTCCCTTTCCGAGAGTTTACAGT 644
 DB 636 ATTATTTGAATCTTCTCCCTAGCAGGCAATTTTCCCTTTCCGAGAGTTTACAGT 695
 QY 645 TTAGAGAGATAGTATGATGAAAAGGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
 DB 696 TTAGAGAGATAGTATGATGAAAAGGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755
 QY 705 GTAGTGTCTGACCTATGAGTAATCCCTTTGCTAGAAAATTTTAAAGAGAGCTGAGC 764
 DB 756 GTAGTGTCTGACCTATGAGTAATCCCTTTGCTAGAAAATTTTAAAGAGAGCTGAGC 815
 QY 765 TTGTTGAACTAGTGTCTGATCTTCATATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 824
 DB 816 TTGTTGAACTAGTGTCTGATCTTCATATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 875
 QY 825 ATGACCTAGAT- GTAAAATTTTATTTATCATCTAG- AAGCCTTGTCTGAGAAAATG 882
 DB 876 ATGACCTAGATGTAATAATTTTATTTATCATCTAGAAAAGCCTTGTCTGAGAAAATG 935
 QY 883 AATAAATATGAGAGTTTC 902
 DB 936 AATAAATATGAGAGTTTC 955

RESULT 10
 LOCUS B0881763 921 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT 7978342 lupski dorsal root ganglion Homo sapiens cDNA
 accession B0881763
 version B0881763.1 GI:22273771
 keywords EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 921)
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LHAM3575 row: 9 column: 11
 High quality sequence stop: 670.
 Location/Qualifiers
 1..921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6185122"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski dorsal root ganglion"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCGACGCGTCG-3' and
 5'-GACTGATCTGATGCGGAGCGGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

ORIGIN
 Query Match 38.3%; Score 801; DB 13; Length 921;
 Best Local Similarity 98.8%; Pred. No. 1.6e-121;
 Matches 848; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
 QY 112 CGCTTTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTCA 171
 DB 28 CACTTTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTCA 87
 QY 172 GTAACTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTCA 231
 DB 88 GTAACTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTCA 147
 QY 232 CATACCCGCTGACTCAATTTCTCTAGTATGATTAATGCTTTAAGTAGATGAGTGC 291
 DB 148 CATACCCGCTGACTCAATTTCTCTAGTATGATTAATGCTTTAAGTAGATGAGTGC 207
 QY 292 CAAGGAGACTGTGTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 351
 DB 208 CAAGGAGACTGTGTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 267
 QY 352 GATTATTTGTTGTTGATGTCCTGTACACAGCATTTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
 DB 268 GATTATTTGTTGTTGATGTCCTGTACACAGCATTTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
 QY 412 ATTATTTTCCAAAGAGTAATGACATGCAAAAGTTTCAATTAATACTGGGCAATTAAACA 471
 DB 328 ATTATTTTCCAAAGAGTAATGACATGCAAAAGTTTCAATTAATACTGGGCAATTAAACA 367
 QY 472 ATAAATTAATTAATAGATTCCTCTGAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 531
 DB 388 ATAAATTAATTAATAGATTCCTCTGAGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 447

QY 532 ACAATTGAGATCGTTGAAAAAGCTAGTATATTTTCAGAGAAATGATTTTCATTATTG 591
DB 448 ACAAAATTGAGATCGTTGAAAAAGCTAGTATATTTTCAGAGAAATGATTTTCATTATTG 507
QY 592 AAACGTCTCCCTAGCAGGCCATTTCCCTTTTCTGGAGTTAGCAAGTTTAGAG 651
DB 508 AAACGTCTCCCTAGCAGGCCATTTCCCTTTTCTGGAGTTAGCAAGTTTAGAG 567
QY 652 AGAATGTCATGAAAAAGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 711
DB 568 AGAATGTCATGAAAAAGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
QY 712 CTCAGACCTATGACGTAATCCCTGCTAGAGAAATTTTAAAGAGAGAGAGAGAGAGAG 771
DB 628 CTCAGACCTATGACGTAATCCCTGCTAGAGAAATTTTAAAGAGAGAGAGAGAGAGAG 687
QY 772 AAACGTAGTTTGTGATCTTCATATTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
DB 688 AAACGTAGTTTGTGATCTTCATATTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 747
QY 832 TAGATGTAATTTTATTTTATTCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 891
DB 748 TAGATGTAATTTTATTTTATTCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806
QY 892 TGAGGGTTTCCTGTCATATCT-GGCTTGCATGTGC-AGAGAGAGAGAGAGAGAGAG 949
DB 807 TGAGGGTTTCCTGTCATATCTGGGCTTGCATGTGCAGAGAGAGAGAGAGAGAGAG 866
QY 950 TAA-TCTCCAGATCCAA 966
DB 867 TAATCTCCAGATCCAA 884

RESULT 11
BI752648 880 bp mRNA linear EST 25-SEP-2001
LOCUS 603021702F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192376 5',
DEFINITION mRNA sequence.
ACCESSION BI752648
VERSION BI752648.1 GI:15744226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 880)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN ac:
http://image.llnl.gov
plate: LLN11481 row: c column: 01
High quality sequence stop: 795.
Location/Qualifiers
1. 880
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5192376"
/lab_host="DH10B"
/clone_1fb="NIH MGC 114"
/note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains; age range 23-27 yo. library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."

Query Match 38.1%; Score 796; DB 12; Length 880;
Best Local Similarity 98.0%; Pred. No. 1,1e-120;
Matches 816; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1230 CAGCATCCTTACACATCCCAAACTAAAGATCACTCTTCCAACTGAGAAAGACTC 1289
DB 1 CAGCATCCTTACACATCCCAAACTAAAGATCACTCTTCCAACTGAGAAAGACTC 60
QY 1290 CTGGCTTTGATGAGAACTTACAGCAGAGAGTCAAGGCCACGCAACAAAGACAC 1349
DB 61 CTGGCTTTGATGAGAACTTACAGCAGAGAGTCAAGGCCACGCAACAAAGACAC 120
QY 1350 AACAACTTTGGAAATATATTTCTCAACCTGATTTATATATATATATATTTTTC 1409
DB 121 AACAACTTTGGAAATATATTTCTCAACCTGATTTATATATATATATATTTTTC 180
QY 1410 TAGTAGAGAACTPACAAATGAGCTCTTCAACTTATATATACGTTTATATAGCTCTTG 1469
DB 181 TAGTAGAGAACTPACAAATGAGCTCTTCAACTTATATATATATATATATATAGCTCTTG 240
QY 1470 CAAGTTCTGTTCTGCTCACTGAGGATTTTTCCTCCGCACTGGCCCTGTTCTCTC 1529
DB 241 CAAGTTCTGTTCTGCTCACTGAGGATTTTTCCTCCGCACTGGCCCTGTTCTCTC 300
QY 1530 CCTTCCTCTTCTCCTTTTGGAGAGAAATATTTTAAATTTGGTCCAACTTCAATTA 1589
DB 301 CCTTCCTCTTCTCCTTTTGGAGAGAAATATTTTAAATTTGGTCCAACTTCAATTA 360
QY 1590 TGTAAATATTAATACATTAATAAGCATTTTACCTTCTTCTGAGAAATGACAGGGCTAG 1649
DB 361 TGTAAATATTAATACATTAATAAGCATTTTACCTTCTTCTGAGAAATGACAGGGCTAG 420
QY 1650 GCATAGACAAAGAGAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGCATCTGAAT 1709
DB 421 GCATAGACAAAGAGAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGCATCTGAAT 480
QY 1710 AAATATTTGGCAAAAGTCTTTTATATGCTATATATATATATATATATATATATAT 1769
DB 481 AAATATTTGGCAAAAGTCTTTTATATGCTATATATATATATATATATATATATAT 539
QY 1770 TTTTATATGTTGCAACTAGCACTCATCTCGGAGACACAGCCAGAGAGATGAGTAGA 1829
DB 540 TTTTATATGTTGCAACTAGCACTCATCTCGGAGACACAGCCAGAGAGATGAGTAGA 599
QY 1830 AGTGAAGAGTTTAAATCCATTTGTAAGCATTTATTCATATTTTAAATTCAGAGAA 1889
DB 600 AGTGAAGAGTTTAAATCCATTTGTAAGCATTTATTCATATTTTAAATTCAGAGAA 659
QY 1890 AATTGAGTTATCTTGAAGATTTTGTATTCATATCTTATATATATATATATATATAT 1949
DB 660 AATTGAGTTATCTTGAAGATTTTGTATTCATATCTTATATATATATATATATATAT 719
QY 1950 CTGGATTAATTAAGACCAAAATGTATCTGTATACCAATCCACATATATATATATAT 2009
DB 720 CTGGATTAATTAAGACCAAAATGTATCTGTATACCAATCCACATATATATATATAT 779
QY 2010 ATATATCTATATACAGCCCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2062
DB 780 ATATATCTATATACAGCTCNAATTAATTAATTAATTAATTAATTAATTAATTAAT 832

RESULT 12
AL523086/c 1168 bp mRNA linear EST 22-MAY-2003
LOCUS AL523086 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS00C001YH21 3-PRIME, mRNA sequence.

ACCESSION AL523086
 VERSION AL523086.2 GI:31041347
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1168)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization.
 Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:12786579.
 COMMENT
 Contact: Genoscope - Centre National de Sequencage
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 379.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC001CD1INP1&cluster=379.r. Contact : Feng Liang Email : fliang@life.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC001CD1INP1.
 Location/Qualifiers

FEATURES
 source 1..1168
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="CS0DC001YH21"
 /issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_1b="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 37.5%; Score 783.4; DB 9; Length 1168;
 Best Local Similarity 91.8%; Pred. No. 1e-118;
 Matches 809; Conservative 11; Mismatches 61; Indels 0; Gaps 0;

QY 1132 GTTACATTTAGACGCTACTGTTGTGTTAAACACACTTTTACCAATAGCTTGAG 1191
 DB 881 GATTAACAATTTGGCGGCTACTGTTGTGTTAAACACACTTTTACCAATAGCTTTAG 822
 QY 1192 GCAACGAGAGCACTACTATTAAAGAAAGGTTTCCAGATCATCTACATCCCA 1251
 DB 821 GSAACGAGGGAATGACTATTAAAGAAAGGTTTCCAGATCATCTACATCCCA 762
 QY 1252 AACTAAAAGATCACTCTTCCAACTGAGAAAAGACTCTGCTTGAATGGAACCTTAC 1311
 DB 761 GACTAAAGAGGTCACTCTTCCGACTGAGARAGACTCTGCTTGAATGAGARACTGAC 702
 QY 1312 AGCAGAGGTCAGAGGCCACGCAACAAGACAGCAACAACAATTTGAATTTAAT 1371
 DB 701 VGGARAGATTTAAGGCCACCGCACACACACACACACACATTTGGAATTTAAT 642
 QY 1372 CTCACATCAAGTTTATATACATCTTATATTTTCTAGTAGAGAAATCAATCAG 1431
 DB 641 CTCACATCAAGTTTATATACATCTTATATTTTCTAGTAGAGAAATCAATCAG 582
 QY 1432 CCTCTTCACTTATATACAGTTTAAAGCTCTTGAAGTACTTGTCTCAGCT 1491
 DB 581 CCTCTTCACTTATATACAGTTTAAAGCTCTTGAAGTACTTGTCTCAGCT 522
 QY 1492 GAGGATATTTTCTCCCACTTGCCTGCTCTCTCCCTCTCTCTCTCTCTCTCTGCA 1551
 DB 521 TAGGATATTTTCTCCCACTTGCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTGCA 462
 QY 1552 GAGGATATTTTAACTATTTGGGTGCACTTAAATAGTAAATTAATTAATTAATAA 1611
 DB 461 GAGGATATTTTAACTATTTGGGTGCACTTAAATAGTAAATTAATTAATTAATAA 402

QY 1612 GCATTTACTCTCTTTCTGAAAAATGCAAGGCTAAGCATAGACAAACAAAGGAAA 1671
 DB 401 GCATTTACTCTCTCTTTCTGAAAAATGCAAGGCTAAGCATAGACAAACAAAGGAAA 342
 QY 1672 TGCTGAGAAATTTGCGACGAGGAGAGACAGCAATGTGAATTAATTTGCCAAAAGTCTT 1731
 DB 341 TGCTGAGAAATTTGCGACGAGGAGAGACAGCAATGTGAATTAATTTGCCAAAAGTCTT 282
 QY 1732 TTATGTCATATAGTGTGAGATTTGAAGAGCTATTTTTTTTAAATGTTGCAATGCA 1791
 DB 281 TTTTTCATATAGTGTGAGATTTGAAGAGCTATTTTTTTTAAATGTTGCAATGCA 222
 QY 1792 CTATCTTGGAGAGACAGCCGAGCATGAGTAAAGTAAAGTTATTAATCCAT 1851
 DB 221 MTATCTTGGGAAAAACGCGAGGAAGTGAAGTGAAGGTTTATTAATCCAT 162
 QY 1852 TTGTAAAGCATTTTCCCATATTTTAAATTCAGAAAAATGTGTTATCTTTAGAAAT 1911
 DB 161 TTGTAAAGCATTTTCCCATATTTTAAATTCAGAAAAATGTGTTATCTTTAGAAAT 102
 QY 1912 TTGTATTCATCTTTTATGACTAGTACTGATGCTTCTGATTAATAAGACCAAT 1971
 DB 101 TTGTATTCATCTTTTATGACTAGTACTGATGCTTCTGATTAATAAGACCAAT 42
 QY 1972 ATGATCTGTACACATCAGATATTAATTAATAATA 2012
 DB 41 ATGATCTGTACACATCAGATATTAATTAATAATA 1

RESULT 13
 BQ720852 841 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOUR 8241231 lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6187117 5', mRNA sequence.
 ACCESSION BQ720852
 VERSION BQ720852.1 GI:21859749
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 841)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM3580 row: j column: 14
 High quality sequence stop: 700.
 Location/Qualifiers

FEATURES

source

1..841
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6187117"
 /sex="male"
 /issue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_1b="lupski_sympathetic_trunk"
 /note="Vector: pCMVSPORT6 (Life Technologies); Site: 1: NotI; site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCACCATGCGGTCCG-3' and 5'-GACTAGTTTCAATCGAGCGGCCCTT(15)-3'. Size selected >

ORIGIN

1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

Query Match 37.1%; Score 775.4; DB 13; Length 841;
Best Local Similarity 97.2%; Pred. No. 2.5e-117;
Matches 805; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

```

OY 77 CTTGAGCATGTAATTAATCTTCATCTTCCCGCCG-----CTTTTG 120
DB 1 CTTGAGCATGTAATTAATCTTCATCTTCCCGCCGACATACACACACACTTTTG 60
OY 121 TTTCTTTAGGTAGACACCTTTTAAAGCAACTACTAGGACATTTCTAGTACTTG 180
DB 61 TTTCTTTAGGTAGACACCTTTTAAAGCAACTACTAGGACATTTCTAGTACTTG 120
OY 181 CTTTCAATCAATAAAGTCAATGATGGAACATTTGTGCTCTCTCATACCCCG 240
DB 121 CTTTCAATCAATAAAGTCAATGATGGAACATTTGTGCTCTCTCATACCCCG 180
OY 241 TGTACTCAATTTCTACTGTATGATTAATCTTTAAGTATGATTCAGTCCAGAGAA 300
DB 181 TGTACTCAATTTCTACTGTATGATTAATCTTTAAGTATGATTCAGTCCAGAGAA 240
OY 301 CTTGGTGAATTAATTAATTTTATTTTTCCTTTAACAAGCATGATTTAT 360
DB 241 CTTGGTGAATTAATTAATTTTATTTTTCCTTTAACAAGCATGATTTAT 300
OY 361 TGGTTGATGTGTCTCTGTACACAGCCATTTCAATAGATGAGCTGTATTTTTC 420
DB 301 TGGTTGATGTGTCTCTGTACACAGCCATTTCAATAGATGAGCTGTATTTTTC 360
OY 421 CAAAGAGTATAGACATGCAAAAGTTTCAATAAAGTGGCCCTTAACAATAATTA 480
DB 361 CAAAGAGTATAGACATGCAAAAGTTTCAATAAAGTGGCCCTTAACAATAATTA 420
OY 481 TAAACTATTAAGATTCCTCTAGGTTTTGCCAACTGCTATCCATTAACAATTTG 540
DB 421 TAAACTATTAAGATTCCTCTAGGTTTTGCCAACTGCTATCCATTAACAATTTG 480
OY 541 AGAATCGTTGAAAAAGCTAGTATATTTCAGAGAAAGATTTTATTTGAATCTTC 600
DB 481 AGAATCGTTGAAAAAGCTAGTATATTTCAGAGAAAGATTTTATTTGAATCTTC 540
OY 601 TCCCTAGAGGCAATTTTCCCTTTTCTGAGAGTTTAGCAAGTTTAGAGAGATAGTC 660
DB 541 TCCCTAGAGGCAATTTTCCCTTTTCTGAGAGTTTAGCAAGTTTAGAGAGATAGTC 600
OY 661 ATGAAAAGAAAGGAAAGGAGGAGAGAGAGGATTAATAAGTAAAGTCTCAGACCT 720
DB 601 ATGAAAAGAAAGGAAAGGAGGAGAGAGAGGATTAATAAGTAAAGTCTCAGACCT 660
OY 721 ATGAAAGTAAATCCCTTGTCTAGAAATTTTAAGAGAGCTCAGCTGTTGAAGT 780
DB 661 ATGAAAGTAAATCCCTTGTCTAGAAATTTTAAGAGAGCTCAGCTGTTGAAGT 720
OY 781 TTTGTCAATCTTCATTTTGGAGAGAGATTTTCTAGCTTGAATGCAATGATGTAA 840
DB 721 TTTGTCAATCTTCATTTTGGAGAGAGATTTTCTAGCTTGAATGCAATGATGTAA 780
OY 841 AATTTTATTTATCATCTAGAAAGCCTTGAAGTAAATGAAATTA 888
DB 781 AATTTTATTTATCATCTAGAAAGCCTTGAAGTAAATGAAATTA 828

```

RESULT 14

BUS68349 797 bp mRNA linear EST 16-SEP-2002
LOCUS BUS68349
DEFINITION AGSCOURT_1040538 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:661581
5', mRNA sequence.

ACCESSION BUS68349
VERSION BUS68349.1 GI:22518649
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLES Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>

Plate: LLCW2857 row: f column: 21
High quality sequence stop: 566.
Location/Qualifiers

FEATURES

source
1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:661581"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lib="NIH_MGC_82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI (ggccatcagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTAAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGACGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 36.2%; Score 757.8; DB 13; Length 797;
Best Local Similarity 96.3%; Pred. No. 2e-114;
Matches 765; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

OY 1273 CAATGAGAAAGACTCTCGGCTTGAATGAGAACTTACAGAGAGTCAAGGCCACG 1332
DB 3 CAATGAGAAAGACTCTCGGCTTGAATGAGAACTTACAGAGAGTCAAGGCCACG 62
OY 1333 GCAACACACAGACAAACAAACATTTGGAATATTATTCTCACTCAGTTTAAT 1392
DB 63 GCAACACACAGACAAACAAACATTTGGAATATTATTCTCACTCAGTTTAAT 122
OY 1393 ACATCTTATTTTCTAGTAGAGAACTCAATCAGCCTCTCAACATTTATATCA 1452
DB 123 ACATCTTATTTTCTAGTAGAGAACTCAATCAGCCTCTCAACATTTATATCA 182
OY 1453 GTTATATAAGCTCTGGAAGTACTGTCTTCTCAGCTGAGATTTTTTCTCCCA 1512
DB 183 GTTATATAAGCTCTGGAAGTACTGTCTTCTCAGCTGAGATTTTTTCTCCCA 242
OY 1513 CTTGCCCCCTGTTCTCCCTTCTCTTCCCTTGAAGAGAAATTTAAACATATT 1572
DB 243 CTTGCCCCCTGTTCTCCCTTCTCTTCCCTTGAAGAGAAATTTTAACATATT 302
OY 1573 GGGTCAACTCAATATGTAATTAATTAATTAATTAATTAATTAATTAATTA 1632
DB 303 GGGTCAACTCAATATGTAATTAATTAATTAATTAATTAATTAATTAATTA 362
OY 1633 AAAATGCAAGGCTTAAGCATTAAGCAAAAGAGAAATGCTAGAAATTTGCCACTGG 1692
DB 363 AAAATGCAAGGCTTAAGCATTAAGCAAAAGAGAAATGCTAGAAATTTGCCACTGG 422

```

QY 1693 AGACAGCAATCTGATATAATTTGGCAAAAGTCTTTTATGTCATATAGTGTGAGA 1752
 DB 423 AGACAGCAATCTGATATAATTTGGCAAAAGTCTTTTATGTCATATAGTGTGAGA 482
 QY 1753 TTTGAGAGAGCTATTTTTTTTAAATGTTGCAACTGACACTCATCTTGGAGACAGC 1812
 DB 483 TTTGAGAGAGCTATTTTTTTTAAATGTTGCAACTGACACTCATCTTGGAGACAGC 542
 QY 1813 CAGGAGATGAGTGAAGTGAAGCTTAAATCACTTTGTAGATTTATCCCAT 1872
 DB 543 CAGGAGATGAGTGAAGTGAAGCTTAAATCACTTTGTAGATTTATCCCAT 602
 QY 1873 ATTTAAATTCAGAAAAATTTGTTTATCTTTAGATTTTGTATTCATCTTATGTA 1932
 DB 603 ATTTAAATTCAGAAAAATTTGTTTATCTTTAGATTTTGTATTCATCTTATGTA 662
 QY 1933 CATGTGACTCATGCTTCTGATTAATAAGACCAATATGTCGTACCAATCA 1992
 DB 663 CATGTGACTCATGCTTCTGATTAATAAGACCAATATGTCGTACCAATCA 722
 QY 1993 CACATATATATTAATATATATCTATATTAACAGCCAAAAAAGAGAGAGAA 2052
 DB 723 CACATATATATTAATATATATCTATATTAACAGCCAAAAAAGAGAGAGAA 782
 QY 2053 AAAGAAGAGAGAG 2066
 DB 783 ANNNAAAAACATG 796

RESULT 15
 BI752817 795 bp mRNA 1linear EST 25-SEP-2001
 LOCUS 603022001P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192352 5',
 DEFINITION mRNA sequence.
 ACCESSION BI752817
 VERSION BI752817.1 GI:15744395
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bts-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNM at:
 http://image.llnl.gov
 Plate: LLM11481 row: b column: 01
 High quality sequence stop: 792.
 Location/Qualifiers
 1..795
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5192352"
 /lab_host="DH10B"
 /note="Torgan: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:

ORIGIN this is a NIH_MGC Library."
 Query Match 35.0%; Score 732.4; DB 12; Length 795;
 Best Local Similarity 98.7%; Pred. No. 2,8e-110;
 Matches 780; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

QY 1230 CAGCATCACTTACATCCCAAACTAAAGATCAACTCTTCCACTGAGAAAAGACTC 1289
 DB 1 CAGCATCACTTACATCCCAAACTAAAGATCAACTCTTCCACTGAGAAAAGACTC 60
 QY 1290 CTGGCTTTGAATGGAACCTTAACAGAGAGTCAAGGCCAGGCAACAGCAAC 1349
 DB 61 CTGGCTTTGAATGGAACCTTAACAGAGAGTCAAGGCCAGGCAACAGCAAC 120
 QY 1350 AACAAACATTTGGAATATATTTCTCACTCAGCTTTTAAATATACATCTTATATTTTC 1409
 DB 121 AACAAACATTTGGAATATATTTCTCACTCAGCTTTTAAATATACATCTTATATTTTC 180
 QY 1410 TAGTAGAGAACTCAAAATCAGCTCTTCAATTTATACAGTTTAAAGCCTCTTG 1469
 DB 181 TAGTAGAGAACTCAAAATCAGCTCTTCAATTTATACAGTTTAAAGCCTCTTG 240
 QY 1470 CAAGTACTGTTCTCTGCACTGAGATTTTTCCTCCCACTGCGCTGTTCTC 1529
 DB 241 CAAGTACTGTTCTCTGCACTGAGATTTTTCCTCCCACTGCGCTGTTCTC 300
 QY 1530 CCTTCCTCTCTCTCTCTGCAAGAGAAATTTTAAATTTGGTCCACTTCAATTA 1589
 DB 301 CCTTCCTCTCTCTCTCTGCAAGAGAAATTTTAAATTTGGTCCACTTCAATTA 360
 QY 1590 TGTAAATTA-TTAAATATTAAGATTTAACTCTCTCTCTGAAATAATGACAGGCTAA 1648
 DB 361 TGTAAATTAATTAATTAATTAAGATTTAACTCTCTCTCTGAAATAATGACAGGCTAA 420
 QY 1649 GGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGATCTGAA 1708
 DB 421 GGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGATCTGAA 480
 QY 1709 TAAATTTTGGCCAAAAGTCTTTTATGTCATATATAGTGCAGATTTGAGAGAGCTATT 1768
 DB 481 TAAATTTTGGCCAAAAGTCTTTTATGTCATATATAGTGCAGATTTGAGAGAGCTATT 539
 QY 1769 TTTTAAATGTTGCACTGCAACTCATCTTGGAGACAGCCAGAGAAATGAAGTAG 1828
 DB 540 TTTTAAATGTTGCACTGCAACTCATCTTGGAGACAGCCAGAGAAATGAAGTAG 599
 QY 1829 AAGTGAAGGTTTAAATCAATCTTGTGAAGCATTTATCCCATATATTTAAATTCAGAA 1888
 DB 600 AAGTGAAGGTTTAAATCAATCTTGTGAAGCATTTATCCCATATATTTAAATTCAGAA 659
 QY 1889 AAATGAGTTTATCTTGAAGTTTGTATTCAA-TACTTATGACTATGTGACTCATGC 1947
 DB 660 AAATGAGTTTATCTTGAAGTTTGTATTCAAAGTACTTTATGACTATGTGACTCATGC 718
 QY 1948 TTCTGATTAATTAAGACCAATATGATCTGTAACCAATCACTATATTTATTA 2007
 DB 719 TTCTGATTAATTAAGACCAATATGATCTGTAACCAATCACTATATTTATTA 778
 QY 2008 ATATATATCT 2017
 DB 779 ATATATATCT 788

Search completed: May 5, 2004, 17:58:49
 Job time : 5411 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 16:28:49 ; Search time 861 Seconds
(without alignments)
10985.556 Million cell updates/sec

Title: US-09-646-569a-60

Perfect score: 2091
Sequence: 1 aagagacagacttaactc.....ggagagaagggg99999999gt 2091

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues
Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgnt2_6/ptodata/2/pubna/US07_PUBCOMB.seq.*
- 2: /cgnt2_6/ptodata/2/pubna/PCT_NEW_PUB.seq.*
- 3: /cgnt2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
- 4: /cgnt2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
- 5: /cgnt2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
- 6: /cgnt2_6/ptodata/2/pubna/PCTUS_PUBCOMB.seq.*
- 7: /cgnt2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
- 8: /cgnt2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
- 9: /cgnt2_6/ptodata/2/pubna/US09_PUBCOMB.seq.*
- 10: /cgnt2_6/ptodata/2/pubna/US09_PUBCOMB.seq.*
- 11: /cgnt2_6/ptodata/2/pubna/US09C_PUBCOMB.seq.*
- 12: /cgnt2_6/ptodata/2/pubna/US09_NEW_PUB.seq.*
- 13: /cgnt2_6/ptodata/2/pubna/US09_NEW_PUB.seq.2.*
- 14: /cgnt2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
- 15: /cgnt2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
- 16: /cgnt2_6/ptodata/2/pubna/US10C_PUBCOMB.seq.*
- 17: /cgnt2_6/ptodata/2/pubna/US10_NEW_PUB.seq.*
- 18: /cgnt2_6/ptodata/2/pubna/US10_NEW_PUB.seq.*
- 19: /cgnt2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2003.8	95.8	3674	10	US-09-984-271-73 Sequence 73, Appl
2	2003.8	95.8	3674	13	US-09-984-276-73 Sequence 73, Appl
3	2001.8	95.7	5809	13	US-10-133-013-103 Sequence 103, App
4	1878.6	89.8	1909	13	US-09-918-715-268 Sequence 268, App
5	1878.6	89.8	1909	16	US-10-341-434-223 Sequence 223, App
6	1853.4	89.6	6005	17	US-10-641-643-341 Sequence 341, App
7	472.8	22.6	500	13	US-10-085-783A-2431 Sequence 2431, A
8	472.8	22.6	500	16	US-10-242-535A-2431 Sequence 2431, A
9	439.6	21.0	466	13	US-10-085-783A-36782 Sequence 36782, A
10	439.6	21.0	466	16	US-10-242-535A-36782 Sequence 36782, A
11	389.8	18.6	460	13	US-10-085-783A-20216 Sequence 20216, A
12	389.8	18.6	460	16	US-10-242-535A-20216 Sequence 20216, A
13	364	17.4	400	13	US-10-085-783A-22085 Sequence 22085, A
14	364	17.4	400	16	US-10-242-535A-22085 Sequence 22085, A

C 15	331	15.8	331	9	US-09-954-456-2136	Sequence 2136, Ap
C 16	331	15.8	331	9	US-09-880-107-1360	Sequence 1360, Ap
C 17	331	15.8	331	10	US-09-872-367C-633	Sequence 633, App
C 18	178.8	8.6	182	13	US-10-085-783A-19196	Sequence 19196, A
C 19	178.8	8.6	182	16	US-10-242-535A-19196	Sequence 19196, A
C 20	131.4	6.3	133	13	US-10-085-783A-40238	Sequence 40238, A
C 21	131.4	6.3	133	16	US-10-242-535A-40238	Sequence 40238, A
C 22	95.2	4.6	547	9	US-09-917-800A-765	Sequence 765, App
C 23	65.4	3.1	301	9	US-09-759-143-280	Sequence 280, App
C 24	65.4	3.1	301	9	US-09-780-656-280	Sequence 280, App
C 25	65.4	3.1	301	9	US-09-822-827-280	Sequence 280, App
C 26	65.4	3.1	301	9	US-09-732-880-280	Sequence 280, App
C 27	65.4	3.1	301	9	US-09-895-793-280	Sequence 280, App
C 28	65.4	3.1	301	9	US-09-895-814-280	Sequence 280, App
C 29	65.4	3.1	301	14	US-10-012-886-280	Sequence 280, App
C 30	65.4	3.1	301	15	US-10-010-940-280	Sequence 280, App
C 31	65.4	3.1	301	15	US-10-144-678A-280	Sequence 280, App
C 32	65.4	3.1	301	15	US-10-294-025-280	Sequence 280, App
C 33	60	2.9	60	10	US-09-908-975-16805	Sequence 16805, A
C 34	59	2.8	756	10	US-09-814-353-6226	Sequence 6226, Ap
C 35	58.6	2.8	5102	17	US-10-240-589C-83	Sequence 83, Appl
C 36	58.6	2.8	3673778	15	US-10-312-841-2	Sequence 2, Appl
C 37	58.6	2.8	281	10	US-09-814-353-17383	Sequence 17383, A
C 38	58	2.8	19653	15	US-10-311-455-1307	Sequence 1307, Ap
C 39	58	2.8	751	15	US-10-311-455-1	Sequence 1, Appl
C 40	56.4	2.7	10329	15	US-10-311-455-2096	Sequence 2096, Ap
C 41	56.4	2.7	390	9	US-09-960-352-1976	Sequence 1976, Ap
C 42	55.8	2.6	390	10	US-09-814-353-17808	Sequence 17808, A
C 43	55.2	2.6	580	13	US-10-424-599-73660	Sequence 73660, A
C 44	55.2	2.6	2083	13	US-10-424-599-99586	Sequence 99586, A
C 45	55.2	2.6	2083	13	US-10-424-599-99586	Sequence 99586, A

ALIGNMENTS

RESULT 1
US-09-984-271-73
Sequence 73, Application US/09984271
Publication No. US20030040088A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 3674
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-271-73
Query Match 95.8%; Score 2003.8; DB 10; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 204; Conservative 0; Mismatches 7; Indels 16; Gaps 1;
QY 1 AAGAGACAGACTTAATCACTCAAGTATTAAGACGATGCTTCATGTTATTGTTA 60
DB 1617 AAGAGACAGACTTAATCACTCAAGTATTAAGACGATGCTTCATGTTATTGTTA 1676
QY 61 AAGAGATGATGATAGCTTCAGCATGGAATTAATCTTCATCTCCCGC----- 111

PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 73
LENGTH: 3674
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-276-73

Query Match 95.8%; Score 2003.8; DB 13; Length 3674;
Best Local Similarity 98.9%; Freq. No. 0;
Matches 2034; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

QY 1 AAGAGACAGACTATTAAGTCAAGTAAATTAAGAGAGATGTCATGTTATTTGTA 60
DB 1617 AAGAGACAGACTATTAAGTCAAGTAAATTAAGAGAGATGTCATGTTATTTGTA 1676
QY 61 AAGAGAGTGAATAGCTTCAAGATGTAATATCTTCCACTTCCCGC----- 111
DB 1677 AAGAGAGTGAATAGCTTCAAGATGTAATATCTTCCACTTCCCGC----- 111
QY 112 -----CGTTTGTGTTCTTCAAGTGAACCTTTTAAATGAGAACTAAGTGAAG 164
DB 1737 AAGAGAGTGAATAGCTTCAAGTGAACCTTTTAAATGAGAACTAAGTGAAG 1796
QY 165 CATTCACTGAATCTTGTCTTCAATCAATTAAGTCAATGATGAGAACTTTGTGCC 224
DB 1797 CATTCACTGAATCTTGTCTTCAATCAATTAAGTCAATGATGAGAACTTTGTGCC 1856
QY 225 TACTCTCATACCCCGGTACTCAATCTCTACTGATGATGATGATGATGATGATGAT 284
DB 1857 TACTCTCATACCCCGGTACTCAATCTCTACTGATGATGATGATGATGATGATGAT 1916
QY 285 TCACTGCCAAGAGAACTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 344
DB 1917 TCACTGCCAAGAGAACTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 1976
QY 345 AGCATGATTTTATTTGTTGATGTTGCTCTGTAACAAGCATTTCAATGATGTA 404
DB 1977 AGCATGATTTTATTTGTTGATGTTGCTCTGTAACAAGCATTTCAATGATGTA 2036
QY 405 GCTGTATTTATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGAT 464
DB 2037 GCTGTATTTATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGAT 2096
QY 465 TTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
DB 2097 TTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2156
QY 525 TCCAAATAACAATTTGGAATGCTGTAAGAAAGCTAGTATTAATTTCAAGAAAGATTTTC 584
DB 2157 TCCAAATAACAATTTGGAATGCTGTAAGAAAGCTAGTATTAATTTCAAGAAAGATTTTC 2216
QY 585 ATTAATGAAGCTGTTCTCCAGAGGCAATTTCCCTTTTCCCTGAGATTTAGCAAGT 644
DB 2217 ATTAATGAAGCTGTTCTCCAGAGGCAATTTCCCTTTTCCCTGAGATTTAGCAAGT 2276
QY 645 TTAGAGAGATTAATGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
DB 2277 TTAGAGAGATTAATGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2336
QY 705 GTAAGTCTCAGACCTATGAAGCTAATCCCTTGTCTAGAAATATTTAAGAGAGCTCAGC 764
DB 2337 GTAAGTCTCAGACCTATGAAGCTAATCCCTTGTCTAGAAATATTTAAGAGAGCTCAGC 2396
QY 765 TTGGTTGAACCTGAGTTTGTCAATCTTCAATTTGAGAGAGATTTTCTGACTTGA 824

DB 2397 TTGGTTGAACCTGAGTTTGTCAATCTTCAATTTGAGAGAGATTTTCTGACTTGA 2456
QY 825 ATGCAAGCTAGATGAATTAATTTATTTATTTATCTGAGAAAGCTTGAAGAAATGAA 884
DB 2457 ATGCAAGCTAGATGAATTAATTTATTTATCTGAGAAAGCTTGAAGAAATGAA 2516
QY 885 TAAATATGAGAGTTTCCCTGATATGATGATGATGATGATGATGATGATGATGATGAT 944
DB 2517 TAAATATGAGAGTTTCCCTGATATGATGATGATGATGATGATGATGATGATGATGAT 2576
QY 945 AAATGAATCTTCAACATCAAGATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1004
DB 2577 AAATGAATCTTCAACATCAAGATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2636
QY 1005 TTGAGACAGAAATTTGAGCAATCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1064
DB 2637 TTGAGACAGAAATTTGAGCAATCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2696
QY 1065 GCTTATAGTCTTCAATCTTATGAGACAGCAAGTGAAGCAAGTGAAGTGAAGTGAAG 1124
DB 2697 GCTTATAGTCTTCAATCTTATGAGACAGCAAGTGAAGCAAGTGAAGTGAAGTGAAG 2756
QY 1125 CTCTTATGTTCAATTTAGAGCTACTGTTGTGTTAAACACTTTTACCAATATAG 1184
DB 2757 CTCTTATGTTCAATTTAGAGCTACTGTTGTGTTAAACACTTTTACCAATATAG 2816
QY 1185 TTCTGAGCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1244
DB 2817 TTCTGAGCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2876
QY 1245 ATCCCAAACTAATAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1304
DB 2877 ATCCCAAACTAATAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2936
QY 1305 AACTTACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364
DB 2937 AACTTACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2996
QY 1365 TATTAATCTCAACAGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1424
DB 2997 TATTAATCTCAACAGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3056
QY 1425 AATAGAGCTCTTCAACATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1484
DB 3057 AATAGAGCTCTTCAACATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 3116
QY 1485 CTCACCTGAGATTTTCTTCCCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1544
DB 3117 CTCACCTGAGATTTTCTTCCCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3176
QY 1545 TTTGCAAGAGAAATTTTAATTAATTTGGGTGCTCACTTCAATTAATTAATTAATTAAT 1604
DB 3177 TTTGCAAGAGAAATTTTAATTAATTTGGGTGCTCACTTCAATTAATTAATTAATTAAT 3236
QY 1605 ATTAAGAATTAATCTTCTTCTAGAAATATGCAAGGCTAAGCAATAGCAAAACAA 1664
DB 3237 ATTAAGAATTAATCTTCTTCTAGAAATATGCAAGGCTAAGCAATAGCAAAACAA 3296
QY 1665 AAGAAATGCTAGAAATTTGCACTGAGACAGCAATCTGAATTAATTTTGGCAAAA 1724
DB 3297 AAGAAATGCTAGAAATTTGCACTGAGACAGCAATCTGAATTAATTTTGGCAAAA 3356
QY 1725 GTTCTTTTATGCTCATATAGTGTGAGATTTGAAGAGATTTTATTTAATGTTGCA 1784
DB 3357 GTTCTTTTATGCTCATATAGTGTGAGATTTGAAGAGATTTTATTTAATGTTGCA 3416
QY 1785 CTAGCAATCTCATTTGAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1844
DB 3417 CTAGCAATCTCATTTGAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3476
QY 1845 AATCAATTTGTAGCAATTTATCCATATATTTAATTTCAAGAAATTTGTGTTATCTT 1904

```
Db 3477 AATCATTGTGACATTATCCATATATTTAAATTCAGAAAAATGTGTATCTT 3536
Qy 1905 TAGAATTTTATTCATCTACTTTATGTACTGTAGCTCATGCTTGGATTAATAAG 1964
Db 3537 TAGAATTTTATTCATCTACTTTATGTACTGTAGCTCATGCTTGGATTAATAAG 3596
Qy 1965 ACCAAATATGTATCTGTATACCAATCAACATATATTAATATATATCTATATAC 2024
Db 3597 ACCAAATATGTATCTGTATACCAATCAACATATATTAATATATATCTATATAC 3656
Qy 2025 ACCCAAAAAAATAAAAA 2041
Db 3657 AAAAAAATAAAAAA 3673

RESULT 3
US-10-133-013-103
; Sequence 103, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromolif, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 103
; LENGTH: 5809
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 1330204.51
US-10-133-013-103

Query Match 95.7%; Score 2001.8; DB 15; Length 5809;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 2; Indels 16; Gaps 1;

Qy 1 AAGAGACGACTATTAATCTCCACAGTAAATTAAGACGTATGTCATGTTATTTGTTA 60
Db 3763 AAGAGACGACTATTAATCTCCACAGTAAATTAAGACGTATGTCATGTTATTTGTTA 3822
Qy 61 AAGAGGTGTGAATAGCTTCAAGCATGTGAATATCTTCATCTTCCCGC----- 111
Db 3823 AAGAGGTGTGAATAGCTTCAAGCATGTGAATATCTTCATCTTCCCGCAGACATAC 3882
Qy 112 -----GCTTTTGTGTTCTTTCAGGTAGACACCTTTAAATGACAGAACTAACTGAG 164
Db 3883 AAAAAACAACCTTTTGTGTTCTTTCAGGTAGACACCTTTAAATGACAGAACTAACTGAG 3942
Qy 165 CATTCAGTAACTTTGCTTCAATCAATAAAGTCAAAATGTATGAAAATTTGTGCCC 224
Db 3943 CATTCAGTAACTTTGCTTCAATCAATAAAGTCAAAATGTATGAAAATTTGTGCCC 4002
Qy 225 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAAATTAATGCTTAAGTAGAT 284
Db 4003 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAAATTAATGCTTAAGTAGAT 4062
Qy 285 TCAATGCCAAGAGAACTGTGTAAATTAATTAATTTTATTTTATCTTCAAA 344
Db 4063 TCAATGCCAAGAGAACTGTGTAAATTAATTAATTTTATTTTATCTTCAAA 4122
Qy 345 AGGCATGATTTTATTTGTTGATGTGTCTGTACACAGCCATTTCAATAGATAGA 404
Db 4123 AGGCATGATTTTATTTGTTGATGTGTCTGTACACAGCCATTTCAATAGATAGA 4182
Qy 405 GCTGTAAATTAATTTTCCAAAGAGTAATAGACATGCAAAAGTTTCAATAAAACTGGGCCA 464
```

QY	Db	Sequence	US-09-918-715-268	US-09-918-715-268	US-09-918-715-268
QY	Db	5263	CTCACCCTGAGGATATTTTCTCTCCACCACCTGGCCCTGTCCTCCCTCTCTCC	5322	
QY	Db	1545	TTTGCGAAGAGAAATATTTAAACATATTTGGGCTCACTCAATATATATATATATAC	1604	
QY	Db	5323	TTTCCAGAGAGAAATATATTAACATATTTGGGCTCACTCAATATATATATATATAC	5382	
QY	Db	1605	ATTAAAAACATTTACTCTCTTCTAGAAAAATGACAGGCTAAGGCAATAGACAAAACA	1664	
QY	Db	5383	ATTAAAAACATTTACTCTCTTCTAGAAAAATGACAGGCTAAGGCAATAGACAAAACA	5442	
QY	Db	1665	AGAGAAATGCTGAGAAATTTGCCACTGGAGACAAGCAATCTGAATAAATATTTGCCAAA	1724	
QY	Db	5443	AGAGAAATGCTGAGAAATTTGCCACTGGAGACAAGCAATCTGAATAAATATTTGCCAAA	5502	
QY	Db	1725	GTTCTTTTATATGCTCATATAGTGTGAGATTTGAAGGACTATTTTTTTTAAATGTTGCA	1784	
QY	Db	5503	GTTCTTTTATATGCTCATATAGTGTGAGATTTGAAGGACTATTTTTTTTAAATGTTGCA	5562	
QY	Db	1785	CTAGCAACTCATCTCTCGAAGACACAGCCAGAGAGATAGATAGAGTGAAGGTTTATA	1844	
QY	Db	5563	CTAGCAACTCATCTCTCGAAGACACAGCCAGAGAGATAGATAGAGTGAAGGTTTATA	5622	
QY	Db	1845	AATCCATTTGTAAGCATTTATCCCATATATTTTAAATCAAGAAAAATTGCTTATCTT	1904	
QY	Db	5623	AATCCATTTGTAAGCATTTATCCCATATATTTTAAATCAAGAAAAATTGCTTATCTT	5682	
QY	Db	1905	TAGAAATTTGATTCATACACTTTATGCTATGAGCTCATGCTCTGGATTAATTAAGC	1964	
QY	Db	5683	TAGAAATTTGATTCATACACTTTATGCTATGAGCTCATGCTCTGGATTAATTAAGC	5742	
QY	Db	1965	ACCAATATATGATCTGTATACCAACATCAACATATATATTAATATATATATATAC	2024	
QY	Db	5743	ACCAATATATGATCTGTATACCAACATCAACATATATATATTAATATATATATAC	5802	
QY	Db	2025	AGCCAAA 2031		
QY	Db	5803	AGCCAAA 5809		

Query Match	89.8%	Score 1878.6	DB 13	Length 1909
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1903	Conservative	0	Mismatches 4	Indels 2
Gaps				

Q1	134	GACACCTTTTAAATGACAACTAATGAGGATTCCTAGTACTTGCTTCAATTCAT	193
Db	1	GACACCTTTTAAATGACAACTAATGAGGATTCCTAGTACTTGCTTCAATTCAT	60

QY	194	AAAGTCAAAGTATGAGAAACATTTTGCCCTACCTCCATACACCCCGGCTCAAAATTC	253
Db	61	AAAGTCAAAGTATGAGAAACATTTTGCCCTACCTCCATACACCCCGGCTCAAAATTC	120
QY	254	TCATCTGTATGAATATATGCTTTAAGTAGAATTCAGTGCACAAGAACTTGAGAAATA	313
Db	121	TCATCTGTATGAATATATGCTTTAAGTAGAATTCAGTGCACAAGAACTTGAGAAATA	180
QY	314	ATTATTTTAATTTTTTTTTTAATCCTTTACAAAGCAAGATTTATATTGGTGAATGTG	373
Db	181	ATTATTTTAATTTTTTTTTTAATCCTTTACAAAGCAAGATTTATATTGGTGAATGTG	240
QY	374	CTCTGTACACAGGCATTTCAATAGATGAGAGCTTTAATATTTCMAAGATTAATAG	433
Db	241	CTCTGTACACAGGCATTTCAATAGATGAGAGCTTTAATATTTCMAAGATTAATAG	300
QY	434	ACATGCAAAAGTTTCAATAAAACTGGGCCCTTAACAATTAATTAATACTAATAGC	493
Db	301	ACATGCAAAAGTTTCAATAAAACTGGGCCCTTAACAATTAATTAATACTAATAGC	360
QY	494	ATTCCCTCTAGTGTTTTTCACAACTGCGCTATCCAAATAACAATTGAGATCGTGA	553
Db	361	ATTCCCTCTAGTGTTTTTCACAACTGCGCTATCCAAATAACAATTGAGATCGTGA	420
QY	554	AAGCTAGTTATATTTCAGAGAAATGATTTTCATTATTAATGAACTGTTCCTCCACAGCC	613
Db	421	AAGCTAGTTATATTTCAGAGAAATGATTTTCATTATTAATGAACTGTTCCTCCACAGCC	480
QY	614	ATTTTCCCTTTTCTCGGAGCTTTAGCAAGTTTAGAGAGAAATGTCTATGAAAAGAAAG	673
Db	481	ATTTTCCCTTTTCTCGGAGCTTTAGCAAGTTTAGAGAGAAATGTCTATGAAAAGAAAG	540
QY	674	GAAAGAAAGGGAGAAGGGAAGGTTAAAAAGTAAAGTCTACAGACTATGACGTAAATCC	733
Db	541	GAAAGAAAGGGAGAAGGGAAGGTTAAAAAGTAAAGTCTACAGACTATGACGTAAATCC	600
QY	734	CTTTGCTAGAAATATTTAAGACAGCTCAGCTTGTTGAACCTGAGTTTGTCACTTCC	793
Db	601	CTTTGCTAGAAATATTTAAGACAGCTCAGCTTGTTGAACCTGAGTTTGTCACTTCC	660
QY	794	ATATTGGAGAGAGATATTCTCTACCTGCAATGACAGCTAGATGTAAATTTATTTAT	853
Db	661	ATATTGGAGAGAGATATTCTCTACCTGCAATGACAGCTAGATGTAAATTTATTTAT	720
QY	854	CATCCTAGAAAGCCTTGAATGAAAAATGAATTAATTTAGGGTTTCTGTCCATATCT	913
Db	721	CATCCTAGAAAGCCTTGAATGAAAAATGAATTAATTTAGGGTTTCTGTCCATATCT	780
QY	914	GGCTTGCAATGTCAGAAAGACAGAGATATGAAAAATGTATCTCCAAATCCAGAGATG	973
Db	781	GGCTTGCAATGTCAGAAAGACAGAGATATGAAAAATGTATCTCCAAATCCAGAGATG	840
QY	974	AACCCAAAGGGGTAGGCAATTCATATGAGTTTGGACATGAAGTTGGTGATCTGGTT	1033
Db	841	AACCCAAAGGGGTAGGCAATTCATATGAGTTTGGACATGAAGTTGGTGATCTGGTT	900
QY	1034	TATGTGCTCAATCTGTATTAACCTCTCTGGCTTATAGTCTCTCACTTCTATTAAGCA	1093
Db	901	TATGTGCTCAATCTGTATTAACCTCTCTGGCTTATAGTCTCTCACTTCTATTAAGCA	960
QY	1094	AGCAGGTATCAACACTGTGCTTCCGACACAAGGCTCTTTAGTTAACAATTTAGAGTACTG	1153
Db	961	AGCAGGTATCAACACTGTGCTTCCGACACAAGGCTCTTTAGTTAACAATTTAGAGTACTG	1020
QY	1154	TTTGTGTTAAACAACCTTTTCAACAATAGGTTCTGAGGCAACGAGGCAATGCTAT	1213
Db	1021	TTTGTGTTAAACAACCTTTTCAACAATAGGTTCTGAGGCAACGAGGCAATGCTAT	1080
QY	1214	TAAAGAAAGGCTTTCCAGCATCACTTAACAATCCCAAACTAATAAATCAACTCTTCC	1273
Db	1081	TAAAGAAAGGCTTTCCAGCATCACTTAACAATCCCAAACTAATAAATCAACTCTTCC	1144
QY	1274	AAGTGAAGAAAGACTCTGGCTTTGAATGAACTTACAGCAGAGATCAAGGCCACGG	1333

Db	1141	AACGAGAAAAGACTCCGCTTTGGATGAGAACTTACAGAGAGAGTCAAGGCCACGG	1200
QY	1334	CAACACACAGACAAACAACAAATTTGGAAATATTAATTCACACTCAGCTTTATATATA	1393
Db	1201	CAACACACACACACAAACAACAAATTTGGAAATATTAATTCACACTCAGCTTTATATATA	1260
QY	1394	CATCMT-ATTAATTTTTCAGTAGAGAACTACCAATCAGCTCTTCAACATTATATACA	1452
Db	1261	CATCTTAATTAATTTTTCAGTAGAGAACTACCAATCAGCTCTTCAACATTATATACA	1320
QY	1453	GTTTAATTAAGCCTCTTGCAAGTACTTGTCCTCACCAGGATATTTTTCCTCCCA	1512
Db	1321	GTTTAATTAAGCCTCTTGCAAGTACTTGTCCTCACCAGGATATTTTTCCTCCCA	1380
QY	1513	CCTTGCCCTCTTCTCCTCCTTCTCTCTCTCTTGCAAGGAAATATTAACATATTT	1572
Db	1381	CCTTGCCCTCTTCTCCTCCTTCTCTCTCTTGCAAGGAAATATTAACATATTT	1440
QY	1573	GGGTCCAACTTCATATATGTAATAATATATACATTAATAAGCATTTAACTTCCTTCAGA	1632
Db	1441	GGGTCCAACTTCATATATGTAATAATATATACATTAATAAGCATTTAACTTCCTTCAGA	1500
QY	1633	AAATATGCAAGGCTAAGCATAGACAAACAAGAAATGCTAGAAATTTGCCACTGG	1692
Db	1501	AAATATGCAAGGCTAAGGCATAGACAAACAAGAAATGCTAGAAATTTGCCACTGG	1560
QY	1693	AGACAAGCAATGTGAATTAATTTTGGCCAAAAGTCTTTTATGTCATATAGTGCAGGA	1752
Db	1561	AGACAAGCAATGTGAATTAATTTTGGCCAAAAGTCTTTTATGTCATATAGTGCAGGA	1620
QY	1753	TTTGAAGGAGCTATTTTTTTTTTAAATGTTGCAACTGACACTCATCTTCGAGAGACACGC	1812
Db	1621	TTTGAAGGAGGCTA-TTTTTTTTAAATGTTGCAACTGACACTCATCTTCGAGAGACACGC	1679
QY	1813	CAGGAGAAATGAAGTGAAGTGAAGAGGTTATTAATCCATTTGTAGATTAATCCCATAT	1872
Db	1680	CAGGAGAAATGAAGTGAAGTGAAGAGTTTATTAATCCATTTGTAGATTAATCCCATAT	1739
QY	1873	ATTTTAAATTCAGAAAAAATTTGTGTTATCTTTAGAAATTTGTATCAATACTTATGTA	1932
Db	1740	ATTTTAAATTCAGAAAAAATTTGTGTTATCTTTAGAAATTTGTATCAATACTTATGTA	1799
QY	1933	CTATGTGACTCATGCTTCTGGAATAATAAGACCAAAATAGTATCTGTAACCAACATCA	1992
Db	1800	CTATGTGACTCATGCTTCTGGAATAATAAGACCAAAATAGTATCTGTAACCAACATCA	1855
QY	1993	CACATATTATTAATAATATATATCTATATATACAGCCAAAAAATTTTTAAAAA 2041	
Db	1860	CACATATTATTAATAATATATATCTATATATACAAAAAATTTTTAAAAA 1908	
RESULT 5			
US-10-341-434-223			
; Sequence 223, Application US/10341434			
; Publication No. US20030215835A1			
GENERAL INFORMATION:			
; APPLICANT: Origene Technologies			
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes			
; FILE REFERENCE: 9U 204 205 R1			
; CURRENT APPLICATION NUMBER: US/10/341,434			
; CURRENT FILING DATE: 2003-07-18			
; PRIOR APPLICATION NUMBER: US 60/348,164			
; PRIOR FILING DATE: 2002-01-15			
; PRIOR APPLICATION NUMBER: US 60/348,119			
; PRIOR FILING DATE: 2002-01-15			
; NUMBER OF SEQ ID NOS: 238			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 223			
; LENGTH: 1909			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			

Query Match	89.8%	Score 1878.6	DB 16	Length 1909
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1903	Conservative	0	Mismatches 4	Indels 2
QY 134 GACACCTTTTAAATGACAACTACAGAGCATTTGAGTAACCTTGCTTCAATCAAT	193			
DB 1 GACACCTTTTAAATGACAACTACAGAGCATTTGAGTAACCTTGCTTCAATCAAT	60			
QY 194 AAAGTCAAAATGATAGAAACAATTTGTGCCCTACTCTCCATACCCCGTGAATTC	253			
DB 61 AAAGTCAAAATGATAGAAACAATTTGTGCCCTACTCTCCATACCCCGTGAATTC	120			
QY 254 TCTACTGATGAATTAATGCTTAAGTGAATTCAGTCCCAAGAGAACTTGTAATTA	313			
DB 121 TCTACTGATGAATTAATGCTTAAGTGAATTCAGTCCCAAGAGAACTTGTAATTA	180			
QY 314 ATTAATTTAAATTTTTTTTTATCCCTTACAAAGCCATGATTTATTTGGTATGTGT	373			
DB 181 ATTAATTTAAATTTTTTTTTATCCCTTACAAAGCCATGATTTATTTGGTATGTGT	240			
QY 374 CTCTGTACACAAGCATTTCAATGAGATGAGAGCTGTAATTAATTTCCAAAGTAATAG	433			
DB 241 CTCTGTACACAAGCATTTCAATGAGATGAGAGCTGTAATTAATTTCCAAAGTAATAG	300			
QY 434 ACATGCAAAAGTTTCATTAATAAACTGGGCCATTACAAATTAATTAATAAATTAAGC	493			
DB 301 ACATGCAAAAGTTTCATTAATAAACTGGGCCATTACAAATTAATTAATAAATTAAGC	360			
QY 444 ATTCCCTCTAGGTTTTGGCCAACTGCTATCCAAATACAAATTTGAGATCGTGA	553			
DB 351 ATTCCCTCTAGGTTTTGGCCAACTGCTATCCAAATACAAATTTGAGATCGTGA	420			
QY 554 AAGCTAGTTAATTTACAGAGAAATGATTTGATTAATGAACGTGTCCTCCAGAGCC	613			
DB 421 AAGCTAGTTAATTTACAGAGAAATGATTTGATTAATGAACGTGTCCTCCAGAGCC	480			
QY 614 ATTTTCCCTTTTCTCGGAGTTTACAGAGTTTACAGAGTAATGACATGAAAAAGAGG	673			
DB 481 ATTTTCCCTTTTCTCGGAGTTTACAGAGTTTACAGAGTAATGACATGAAAAAGAGG	540			
QY 674 GAAGAAAGGAGAGAGGAGAGGTTAAAAAGTAAGTGCTCAGACCTATGAACGTATCC	733			
DB 541 GAAGAAAGGAGAGAGGAGAGGTTAAAAAGTAAGTGCTCAGACCTATGAACGTATCC	600			
QY 734 CTTCCTAGAAATATTTAAGAGCAGCTCAAGCTTGATTAACCTAGCTTTTGATCTTCC	793			
DB 601 CTTCCTAGAAATATTTAAGAGCAGCTCAAGCTTGATTAACCTAGCTTTTGATCTTCC	660			
QY 794 AATTTGAGAGAGGATTTTCTAGCTGCAATGAGCTAGATGTAAATTTATTTAT	853			
DB 661 AATTTGAGAGAGGATTTTCTAGCTGCAATGAGCTAGATGTAAATTTATTTAT	720			
QY 854 CATCTGAGAAAGCTTGACTAGTAAAAATGAATTAATTTAGGGTTTTCTGTCCATATCT	913			
DB 721 CATCTGAGAAAGCTTGACTAGTAAAAATGAATTAATTTAGGGTTTTCTGTCCATATCT	780			
QY 914 GGCTTGACATGCTCAGAAAGCAGAGAAATAGAAATGTATCTCCAAATCCAAAGATGGA	973			
DB 781 GGCTTGACATGCTCAGAAAGCAGAGAAATAGAAATGTATCTCCAAATCCAAAGATGGA	840			
QY 974 AACCCAAAGGGATGAGCAATCTATGTAGGTTTTGACATGAAGTTTGGTGCATCTTGTT	1033			
DB 841 AACCCAAAGGGATGAGCAATCTATGTAGGTTTTGACATGAAGTTTGGTGCATCTTGTT	900			
QY 1034 TATGCTGCTCAACCTGCTATTAACCTCTCGAGCTTAATGATCTCTTCATTTCAATAGCA	1093			
DB 901 TATGCTGCTCAACCTGCTATTTAAACCTCTCTGCTTAATGATCTCTTCATTTCAATAGCA	960			

1094 AGCAGTATCGAAGCTTGTCTGCGACAGGCTCTTTAGTTAAATTTAGAGCTACTG 1153
 Db AGCAGTATCGAAGCTTGTCTGCGACAGGCTCTTTAGTTAAATTTAGAGCTACTG 1020
 1154 TTTGTTAAACACACTTTTACCAAAATAGTCTGAGGCAACGAGAGCAATGACTT 1213
 Db TTTGTTAAACACACTTTTACCAAAATAGTCTGAGGCAACGAGAGCAATGACTT 1080
 1214 TAAAGAAAGCTTTCCGACATCTTACATCCCAAACTAAAGATCACTCTTC 1273
 Db TAAAGAAAGCTTTCCGACATCTTACATCCCAAACTAAAGATCACTCTTC 1140
 1274 AACTGAGAAAGACTCTGCTGCTGGAATGAAAGAACTTACAGAGAGACTGACAGCCG 1333
 Db AACTGAGAAAGACTCTGCTGCTGGAATGAAAGAACTTACAGAGAGACTGACAGCCG 1200
 1334 CAACAACAGACAAACAACAATTTGGAATATTATTCTCACTCACTGTTTAAATA 1393
 Db CAACAACAGACAAACAACAATTTGGAATATTATTCTCACTCACTGTTTAAATA 1260
 1394 CATCTT-ATTATTTTCTAGTAAAGAACTCAATCAGCTCTTCAACTTTATATA 1452
 Db CATCTTATTATTTTCTAGTAAAGAACTCAATCAGCTCTTCAACTTTATATA 1320
 1453 GTTTAATAGCTCTTGAAGTACTTGTCTCAGCTGAGTATTTTCTCCCA 1512
 Db GTTTAATAGCTCTTGAAGTACTTGTCTCAGCTGAGTATTTTCTCCCA 1380
 1513 CTTTGCCCTGTCT 1572
 Db CTTTGCCCTGTCT 1440
 1573 GGGTCCAACTTCAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTA 1632
 Db GGGTCCAACTTCAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
 1633 AAAATGCAAGGCTTAAGGATGACAAACAAGAGAAATGCTGAGAAATTTGCCATGG 1692
 Db AAAATGCAAGGCTTAAGGATGACAAACAAGAGAAATGCTGAGAAATTTGCCATGG 1560
 1693 AGACAGAACTGTAATTAATTAATTTGCCAAAGTCTTTATGCTAATAGTCTGAGA 1752
 Db AGACAGAACTGTAATTAATTAATTTGCCAAAGTCTTTATGCTAATAGTCTGAGA 1620
 1753 TTTGAGAGGCTATTTTAAATGTTGAAGTCAAGTCACTCTTCCGAGACAGC 1812
 Db TTTGAGAGGCTATTTTAAATGTTGAAGTCAAGTCACTCTTCCGAGACAGC 1679
 1813 CAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1872
 Db CAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1739
 1873 ATTTAAATTAAGAAATGTTGTTTAAATTTGTAATTTGTAATTTGTAATTTGTA 1932
 Db ATTTAAATTAAGAAATGTTGTTTAAATTTGTAATTTGTAATTTGTAATTTGTA 1799
 1933 CTATGACTCATGCTTCTGGAATTAATTAAGCAACCAATTAATTAATTAATTAATTA 1992
 Db CTATGACTCATGCTTCTGGAATTAATTAAGCAACCAATTAATTAATTAATTAATTA 1859
 1993 CACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2041
 Db CACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1908

RESULT 6
 US-10-641-643-341
 ; Sequence 341, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooke, Benjamin G.
 ; Susan G. Stuart
 ; Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 GENE EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 FILING DATE: 14-Aug-2003
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 341:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6005 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BEPINDON1
 CLONE: 1432736
 SEQUENCE DESCRIPTION: SEQ ID NO: 341 :
 US-10-641-643-341
 Query Match 88.6%; Score 1853.4; DB 17; Length 6005;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 2025; Conservative 0; Mismatches 27; Indels 32; Gaps 13;
 1 AAGAGCAGACTTAACTCCACAGTAAATTAAGACGATGTTCCATGTTATTTGTA 60
 Db AAGAGCAGACTTAACTCCACAGTAAATTAAGACGATGTTCCATGTTATTTGTA 3970
 3911 AAGAGCAGACTTAACTCCACAGTAAATTAAGACGATGTTCCATGTTATTTGTA 3970
 Db AAGAGCAGACTTAACTCCACAGTAAATTAAGACGATGTTCCATGTTATTTGTA 112
 61 AAGCAGTGAATAGCTTCAAGCATGGAATTAATCTTCATCTCCCGCC----- 112
 Db AAGCAGTGAATAGCTTCAAGCATGGAATTAATCTTCATCTCCCGCC----- 4030
 3971 AAGCAGTGAATAGCTTCAAGCATGGAATTAATCTTCATCTCCCGCC----- 4030
 Db AAGCAGTGAATAGCTTCAAGCATGGAATTAATCTTCATCTCCCGCC----- 113
 113 -----GCTTTTGTCTCTTCAAGTGAACCTTTTAAATGACAGACTGAG 164
 Db -----GCTTTTGTCTCTTCAAGTGAACCTTTTAAATGACAGACTGAG 4090
 4031 NNNNNNNNNNTTGTCTTCTTCAAGTGAACCTTTTAAATGACAGACTGAG 4090
 Db NNNNNNNNNNTTGTCTTCTTCAAGTGAACCTTTTAAATGACAGACTGAG 224
 165 CATTTCAGTACTGCTTCTTCAATCAATTAAGTCAATGATGGAACATTTTGTGCC 224
 Db CATTTCAGTACTGCTTCTTCAATCAATTAAGTCAATGATGGAACATTTTGTGCC 4150
 4091 CATTTCAGTACTGCTTCTTCAATCAATTAAGTCAATGATGGAACATTTTGTGCC 4150
 Db CATTTCAGTACTGCTTCTTCAATCAATTAAGTCAATGATGGAACATTTTGTGCC 284
 225 TACTCCATACCCCGTGAATCAATCTCTACTGATGAATTAAGCTTAAAGTAAAT 4210
 Db TACTCCATACCCCGTGAATCAATCTCTACTGATGAATTAAGCTTAAAGTAAAT 4210
 4151 TACTCCATACCCCGTGAATCAATCTCTACTGATGAATTAAGCTTAAAGTAAAT 4210
 Db TACTCCATACCCCGTGAATCAATCTCTACTGATGAATTAAGCTTAAAGTAAAT 343
 285 TCAGTGCCAGAGAGAACTTGTGAATTAATTAATTTTAA-TTTTTTTAAATCTTTTACA 343
 Db TCAGTGCCAGAGAGAACTTGTGAATTAATTAATTTTAA-TTTTTTTAAATCTTTTACA 4270
 4211 TCAGTGCCAGAGAGAACTTGTGAATTAATTAATTTTAA-TTTTTTTAAATCTTTTACA 4270
 Db TCAGTGCCAGAGAGAACTTGTGAATTAATTAATTTTAA-TTTTTTTAAATCTTTTACA 403
 344 AAGCCATGATTTTATTTGTTGATGATGCTGCTGACAGAGCATTTCAATAGATG 403
 Db AAGCCATGATTTTATTTGTTGATGATGCTGCTGACAGAGCATTTCAATAGATG 4330
 4271 AAGCCATGATTTTATTTGTTGATGATGCTGCTGACAGAGCATTTCAATAGATG 4330

Thu May 6 14:19:49 2004

us-09-646-569a-60.rmpb

Page 9

Query Match 22.6%; Score 472.8; DB 13; Length 500;
Best Local Similarity 99.2%; Pred. No. 2e-97;
Matches 485; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1279 AGAAGAACTCTGCTTGGATGAACTTACAGCAGAGACGACGCGGCAACA 1338
12 AAAAAGACTCTGCTTGGATGAACTTACAGCAGAGACGACGCGGCAACA 71
1339 ACAAGCAACAACAACATTTGGAAATATTCTCACTGAGTTTAAATACATCT 1398
72 ACAAGCAACAACAACATTTGGAAATATTCTCACTGAGTTTAAATACATCT 131
1399 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTATATACAGTTTA 1458
132 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTATATACAGTTTA 191
1459 TAAAGCTCTTGAAGTTACTTGTCTCTCACTGAGTTTATTTTCTCCCACTTGC 1518
192 TAAAGCTCTTGAAGTTACTTGTCTCTCACTGAGTTTATTTTCTCCCACTTGC 251
1519 CCTGTTCTCTGCT 1578
252 CCTGTTCTCTGCT 311
1579 AACTTCATTAATGTATATATATATATATATATATATATATATATATATATAT 1637
312 AACTTCATTAATGTATATATATATATATATATATATATATATATATATATAT 371
1638 GCACAGGCTAAGGCTATAGCAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACA 1697
372 GCACAGGCTAAGGCTATAGCAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACA 431
1698 AGCAATCTGAATTAATATTTGGCAAAAGTTCTTTTATGCTATAGTACAGATTGA 1757
432 AGCAATCTGAATTAATATTTGGCAAAAGTTCTTTTATGCTATAGTACAGATTGA 491
1758 AGGAGCTAT 1766
492 AGGAGCTAT 500

RESULT 8

US-10-242-535A-24331
; Sequence 24331, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24331
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)

; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-24331

Query Match 22.6%; Score 472.8; DB 16; Length 500;
Best Local Similarity 99.2%; Pred. No. 2e-97;
Matches 485; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1279 AGAAGAACTCTGCTTGGATGAACTTACAGCAGAGACGACGCGGCAACA 1338
12 AAAAAGACTCTGCTTGGATGAACTTACAGCAGAGACGACGCGGCAACA 71
1339 ACAAGCAACAACAACATTTGGAAATATTCTCACTGAGTTTAAATACATCT 1398
72 ACAAGCAACAACAACATTTGGAAATATTCTCACTGAGTTTAAATACATCT 131
1399 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTATATACAGTTTA 1458
132 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTATATACAGTTTA 191
1459 TAAAGCTCTTGAAGTTACTTGTCTCTCACTGAGTTTATTTTCTCCCACTTGC 1518
192 TAAAGCTCTTGAAGTTACTTGTCTCTCACTGAGTTTATTTTCTCCCACTTGC 251
1519 CCTGTTCTCTGCT 1578
252 CCTGTTCTCTGCT 311
1579 AACTTCATTAATGTATATATATATATATATATATATATATATATATATATAT 1637
312 AACTTCATTAATGTATATATATATATATATATATATATATATATATATATAT 371
1638 GCACAGGCTAAGGCTATAGCAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACA 1697
372 GCACAGGCTAAGGCTATAGCAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACA 431
1698 AGCAATCTGAATTAATATTTGGCAAAAGTTCTTTTATGCTATAGTACAGATTGA 1757
432 AGCAATCTGAATTAATATTTGGCAAAAGTTCTTTTATGCTATAGTACAGATTGA 491
1758 AGGAGCTAT 1766
492 AGGAGCTAT 500

RESULT 9

US-10-085-783A-36782
; Sequence 36782, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36782
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature

LOCATION: (43)..(43)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-36782

Query Match 21.0%; Score 439.6; DB 13; Length 466;
Best Local Similarity 98.7%; Pred. No. 7.1e-90;
Matches 442; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 973 AAACCCAGGGGTAGGCAATTCTATAGATTGGACATGAAGTTGGTGCATCTTGT 1032
DB 14 ANCCCAAGGGGTAGGCAATTCTATAGATTGGACATGAAGTTGGTGCATCTTGT 73
QY 1033 TTAATGCTGCTCAACGCTATTAACTCTGCTTATAGTCTCTTCACTTCTATTAGAC 1092
DB 74 TTAATGCTGCTCAACGCTATTAACTCTGCTTATAGTCTCTTCACTTCTATTAGAC 133
QY 1093 AAGCAGGTATCGAACACTTGTTCGACAAAGGCTCTTTAGTTAACAATTAGACGCTACT 1152
DB 134 AAGCAGGTATCGAACACTTGTTCGACAAAGGCTCTTTAGTTAACAATTAGACGCTACT 193
QY 1153 GTTGTGTTAAACACTTTTCAACAAATAGTTCTGAGGCAAGAGCATATGACTAT 1212
DB 194 GTTGTGTTAAACACTTTTCAACAAATAGTTCTGAGGCAAGAGCATATGACTAT 253
QY 1213 TTAAGAAAGGCTTCCCAACATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 1272
DB 254 TTAAGAAAGGCTTCCCAACATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 313
QY 1273 CAATGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 1332
DB 314 CAATGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 373
QY 1333 GCAACAACAACGACAAACAACATTTGGAATATTCTCAACTCAGCTTTAATAT 1392
DB 374 GCAACAACAACGACAAACAACATTTGGAATATTCTCAACTCAGCTTTAATAT 433
QY 1393 ACATCTTATTATTTTCTAGTAGAGAA 1420
DB 434 ACATCTTATTATTTTCTAGTAGAGAA 461

RESULT 10
US-10-242-535A-36782

Sequence 36782, Application US/10242535A
Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 36782

LENGTH: 466

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (15)..(15)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature

LOCATION: (43)..(43)

OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-36782

Query Match 21.0%; Score 439.6; DB 16; Length 466;
Best Local Similarity 98.7%; Pred. No. 7.1e-90;
Matches 442; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 973 AAACCCAGGGGTAGGCAATTCTATAGATTGGACATGAAGTTGGTGCATCTTGT 1032
DB 14 ANCCCAAGGGGTAGGCAATTCTATAGATTGGACATGAAGTTGGTGCATCTTGT 73
QY 1033 TTAATGCTGCTCAACGCTATTAACTCTGCTTATAGTCTCTTCACTTCTATTAGAC 1092
DB 74 TTAATGCTGCTCAACGCTATTAACTCTGCTTATAGTCTCTTCACTTCTATTAGAC 133
QY 1093 AAGCAGGTATCGAACACTTGTTCGACAAAGGCTCTTTAGTTAACAATTAGACGCTACT 1152
DB 134 AAGCAGGTATCGAACACTTGTTCGACAAAGGCTCTTTAGTTAACAATTAGACGCTACT 193
QY 1153 GTTGTGTTAAACACTTTTCAACAAATAGTTCTGAGGCAAGAGCATATGACTAT 1212
DB 194 GTTGTGTTAAACACTTTTCAACAAATAGTTCTGAGGCAAGAGCATATGACTAT 253
QY 1213 TTAAGAAAGGCTTCCCAACATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 1272
DB 254 TTAAGAAAGGCTTCCCAACATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 313
QY 1273 CAATGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 1332
DB 314 CAATGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 373
QY 1333 GCAACAACAACGACAAACAACATTTGGAATATTCTCAACTCAGCTTTAATAT 1392
DB 374 GCAACAACAACGACAAACAACATTTGGAATATTCTCAACTCAGCTTTAATAT 433
QY 1393 ACATCTTATTATTTTCTAGTAGAGAA 1420
DB 434 ACATCTTATTATTTTCTAGTAGAGAA 461

RESULT 11

US-10-085-783A-20216

Sequence 20216, Application US/10085783A
Publication No. US2004003784LAI

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 20216

LENGTH: 460

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (120)..(120)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature

LOCATION: (301)..(301)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature

LOCATION: (43)..(43)

US-10-085-783A-20216

Query Match 18.6%; Score 389.8; DB 13; Length 460;
 Best Local Similarity 97.0%; Pred. No. 1.6e-78;
 Matches 449; Conservative 0; Mismatches 9; Indels 5; Gaps 5;

1428 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 1486
 1 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 60
 1487 CACCTGAGGATTTTTCCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 1546
 61 CACCTGAGGATTTTTCCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 120
 1547 TCGAAGAGAAATATTTAATATATTTGGGTCCCACTTCAATATATATATATACAT 1606
 121 TCGAAGAGAAATATTTAATATATTTGGGTCCCACTTCAATATATATATATACAT 180
 1607 T-AAAAGCATTTAACTCTCTCTCTCTGAAAATAAGCAAGGCTAAGCATAGACAAA 1665
 181 TAAAAGCATTTAACTCTCTCTCTCTGAAAATAAGCAAGGCTAAGCATAGACAAA 240
 1666 GAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATTTGGCAAAAG 1725
 241 GAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATTTGGCAAAAG 300
 1726 TTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTAAATGTTGCAAC 1785
 301 NTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTAAATGTTGCAAC 360
 1786 TAGCAACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTGAAGTAAAGTTTAA 1845
 361 TAGCAACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTGAAGTAAAGTAAAG-TTATA 418
 1846 ATCCATTGTGAAGCATTTATCCCATATATTTTAAATTCAGAA 1888
 419 ATCCATTGTGAAGC-TTATATCATATATTTTAAATTCAGAA 460

RESULT 12
 US-10-242-535A-20216
 / Sequence 20216, Application US/10242535A
 / Publication No. US20040013663A1
 / GENERAL INFORMATION:
 / APPLICANT: ChondroGene Inc.
 / APPLICANT: Liew, C.C.
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 / FILE REFERENCE: 4231/2005
 / CURRENT APPLICATION NUMBER: US/10/242,535A
 / CURRENT FILING DATE: 2002-09-12
 / PRIOR APPLICATION NUMBER: US 10/085,783
 / PRIOR FILING DATE: 2002-02-28
 / PRIOR APPLICATION NUMBER: US 60/305,340
 / PRIOR FILING DATE: 2001-07-13
 / PRIOR APPLICATION NUMBER: US 60/275,017
 / PRIOR FILING DATE: 2001-03-12
 / PRIOR APPLICATION NUMBER: US 60/271,955
 / PRIOR FILING DATE: 2001-02-28
 / NUMBER OF SEQ ID NOS: 58994
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 20216
 / LENGTH: 460
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (120)..(120)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (301)..(301)
 / OTHER INFORMATION: n is a, c, g, or t
 / US-10-242-535A-20216

Query Match 18.6%; Score 389.8; DB 16; Length 460;

Best Local Similarity 97.0%; Pred. No. 1.6e-78;
 Matches 449; Conservative 0; Mismatches 9; Indels 5; Gaps 5;

1428 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 1486
 1 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 60
 1487 CACCTGAGGATTTTTCCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 1546
 61 CACCTGAGGATTTTTCCTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCT 120
 1547 TCGAAGAGAAATATTTAATATATTTGGGTCCCACTTCAATATATATATATACAT 1606
 121 TCGAAGAGAAATATTTAATATATTTGGGTCCCACTTCAATATATATATATATACAT 180
 1607 T-AAAAGCATTTAACTCTCTCTCTCTGAAAATAAGCAAGGCTAAGCATAGACAAA 1665
 181 TAAAAGCATTTAACTCTCTCTCTCTGAAAATAAGCAAGGCTAAGCATAGACAAA 240
 1666 GAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATTTGGCAAAAG 1725
 241 GAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATTTGGCAAAAG 300
 1726 TTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTAAATGTTGCAAC 1785
 301 NTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTAAATGTTGCAAC 360
 1786 TAGCAACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTGAAGTAAAGTTTAA 1845
 361 TAGCAACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTGAAGTAAAGTAAAG-TTATA 418
 1846 ATCCATTGTGAAGCATTTATCCCATATATTTTAAATTCAGAA 1888
 419 ATCCATTGTGAAGC-TTATATCATATATTTTAAATTCAGAA 460

RESULT 13
 US-10-085-783A-22085
 / Sequence 22085, Application US/10085783A
 / Publication No. US20040037841A1
 / GENERAL INFORMATION:
 / APPLICANT: ChondroGene Inc.
 / APPLICANT: Liew, C.C.
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 / FILE REFERENCE: 4231/2002
 / CURRENT APPLICATION NUMBER: US/10/085,783A
 / CURRENT FILING DATE: 2002-02-28
 / PRIOR APPLICATION NUMBER: US 60/305,340
 / PRIOR FILING DATE: 2001-07-13
 / PRIOR APPLICATION NUMBER: US 60/275,017
 / PRIOR FILING DATE: 2001-03-12
 / PRIOR APPLICATION NUMBER: US 60/271,955
 / PRIOR FILING DATE: 2001-02-28
 / NUMBER OF SEQ ID NOS: 58994
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 22085
 / LENGTH: 400
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (41)..(41)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (64)..(65)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (215)..(216)
 / OTHER INFORMATION: n is a, c, g, or t
 / US-10-085-783A-22085

Query Match 17.4%; Score 364; DB 13; Length 400;
Best Local Similarity 97.2%; Pred. No. 1.1e-72;
Matches 378; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1347 AACACAAACATTGGAAATATTTCTCACTGAGTTTAAATATACATCTTATTT 1406
DB 12 AACCCAAACATTGGAAATATTTCTTCTGAGTTTAAATATACATCTTATTT 71
QY 1407 TTCTAGTAGAAACTACAAATCAGCTCTTCAACATTATATACAGTTTAAAGCTC 1466
DB 72 TTCTAGTAGAAACTACAAATCAGCTCTTCAACATTATATACAGTTTAAAGCTC 131
QY 1467 TTGCAAGTTACTGTTCTCTCACTGAGTATTTTCTCCGCCACCTTGCCCTGTC 1526
DB 132 TTGCAAGTTACTGTTCTCTCACTGAGTATTTTCTCCGCCACCTTGCCCTGTC 191
QY 1527 CTCCTTCCTCTTCTCCCTTTGCAAGAAATATTTAAATATTTGGTCCAACTTCA 1586
DB 192 CTCCTTCCTCTTCTCCCTTTGCAAGAAATATTTAAATATTTGGTCCAACTTCA 251
QY 1587 TAATGTATATTAATTAACATTT-AAAAGCATTTAACTTCTTCTAGAAAAATGCAAGGC 1645
DB 252 TAATGTATATTAATTAACATTTAAAGCATTTAACTTCTTCTAGAAAAATGCAAGGC 311
QY 1646 TAAGCATAGACAAACAAAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCT 1705
DB 312 TAAGCATAGACAAACAAAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCT 371
QY 1706 GAATAAATATTTGCCAAAAGTTCTTTTA 1734
DB 372 GAATAAATATTTGCCAAAAGTTCTTTTA 400

RESULT 14

US-10-242-535A-22085
Sequence 22085, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22085
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (41)..(41)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (64)..(65)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (215)..(216)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-22085

Query Match 17.4%; Score 364; DB 16; Length 400;

Best Local Similarity 97.2%; Pred. No. 1.1e-72;
Matches 378; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1347 AACACAAACATTGGAAATATTTCTCACTGAGTTTAAATATACATCTTATTT 1406
DB 12 AACCCAAACATTGGAAATATTTCTTCTGAGTTTAAATATACATCTTATTT 71
QY 1407 TTCTAGTAGAAACTACAAATCAGCTCTTCAACATTATATACAGTTTAAAGCTC 1466
DB 72 TTCTAGTAGAAACTACAAATCAGCTCTTCAACATTATATACAGTTTAAAGCTC 131
QY 1467 TTGCAAGTTACTGTTCTCTCACTGAGTATTTTCTCCGCCACCTTGCCCTGTC 1526
DB 132 TTGCAAGTTACTGTTCTCTCACTGAGTATTTTCTCCGCCACCTTGCCCTGTC 191
QY 1527 CTCCTTCCTCTTCTCCCTTTGCAAGAAATATTTAAATATTTGGTCCAACTTCA 1586
DB 192 CTCCTTCCTCTTCTCCCTTTGCAAGAAATATTTAAATATTTGGTCCAACTTCA 251
QY 1587 TAATGTATATTAATTAACATTT-AAAAGCATTTAACTTCTTCTAGAAAAATGCAAGGC 1645
DB 252 TAATGTATATTAATTAACATTTAAAGCATTTAACTTCTTCTAGAAAAATGCAAGGC 311
QY 1646 TAAGCATAGACAAACAAAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCT 1705
DB 312 TAAGCATAGACAAACAAAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCT 371
QY 1706 GAATAAATATTTGCCAAAAGTTCTTTTA 1734
DB 372 GAATAAATATTTGCCAAAAGTTCTTTTA 400

RESULT 15

US-09-954-456-2136/c
Sequence 2136, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Car
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2136
LENGTH: 331
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-2136

Query Match 15.8%; Score 331; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 3.2e-65;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1698 AGCAATCTGAATAAATATTGGCCAAAGTCTTTTATATGCAATATAGTGCAGATTGA 1757
|||||
Db 331 AGCAATCTGAATAAATATTGGCCAAAGTCTTTTATATGCAATATAGTGCAGATTGA 272
|||||

QY 1758 AGGAGCTATTTTATATGTTGCACTAGCAACTCATCTTCGGAAGACACAGCCAGGA 1817
|||||
Db 271 AGGAGCTATTTTATATGTTGCACTAGCAACTCATCTTCGGAAGACACAGCCAGGA 212
|||||

QY 1818 GAATGAGTAGAAGTGAAGTTTATAATCCATTGTAGCAATTATCCATATATTT 1877
|||||
Db 211 GAATGAGTAGAAGTGAAGTTTATAATCCATTGTAGCAATTATCCATATATTT 152
|||||

QY 1878 AAATTCAGAAAAATTTGTTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 1937
|||||
Db 151 AAATTCAGAAAAATTTGTTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 92
|||||

QY 1938 TGACTCATGCTTCTGATTAATTAAGCACCAAAATATGTCTGTACCACATCACACAT 1997
|||||
Db 91 TGACTCATGCTTCTGATTAATTAAGCACCAAAATATGTCTGTACCACATCACACAT 32
|||||

QY 1998 ATTATATTAAATATATATCTATATACGCC 2028
|||||
Db 31 ATTATATTAAATATATATCTATATACGCC 1
|||||

Search completed: May 6, 2004, 03:11:12
Job time : 868 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comogen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 14:13:19 ; Search time 154 Seconds
(without alignments)
7535.080 Million cell updates/sec

Title: US-09-646-569a-60

Perfect score: 2091
Sequence: 1 aagagacacacatactc.....ggagagaaggggggagagt 2091

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/6CTUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2003.8	95.8	3674	4	US-09-482-273-73 Sequence 73, Appl
2	1853.4	88.6	6005	4	US-09-023-655-341 Sequence 341, App
3	65.4	3.1	301	4	US-09-439-313-280 Sequence 280, App
4	65.4	3.1	301	4	US-09-352-616A-280 Sequence 280, App
5	65.4	3.1	301	4	US-09-232-149A-280 Sequence 280, App
6	65.4	3.1	301	4	US-09-159-812-280 Sequence 280, App
7	65.4	3.1	301	4	US-09-636-215-280 Sequence 280, App
8	65.4	3.1	301	4	US-09-685-166A-280 Sequence 280, App
9	65.4	3.1	301	4	US-09-688-489-280 Sequence 280, App
10	54.4	2.6	2447	2	US-09-014-962-14 Sequence 14, Appl
11	51.4	2.5	832	4	US-09-621-976-2813 Sequence 2813, App
12	50.2	2.4	7218	1	US-08-232-463-14 Sequence 14, Appl
13	48.8	2.3	1559	4	US-09-489-847-42 Sequence 42, Appl
14	48.4	2.3	169998	4	US-09-676-610B-24 Sequence 24, Appl
15	48.4	2.3	197496	4	US-09-877-177A-10 Sequence 10, Appl
16	47.6	2.3	1664976	4	US-08-916-421B-1 Sequence 1, Appl
17	47.4	2.3	1810	4	US-09-800-723-72 Sequence 72, Appl
18	47.4	2.3	1811	4	US-09-800-723-77 Sequence 77, Appl
19	47.2	2.3	593	4	US-09-904-615-59 Sequence 59, Appl
20	46.8	2.2	1641	1	US-08-300-903A-8 Sequence 8, Appl
21	46.8	2.2	1641	4	US-08-988-197-8 Sequence 8, Appl
22	46.6	2.2	6669	4	US-10-204-708-5 Sequence 5, Appl
23	46.4	2.2	3527	2	US-08-909-965C-7 Sequence 7, Appl
24	46.4	2.2	7218	1	US-08-232-463-14 Sequence 14, Appl
25	46.2	2.2	12141	3	US-09-488-671-10 Sequence 10, Appl
26	45.6	2.2	6124	4	US-08-213-415B-3 Sequence 3, Appl
27	45.6	2.2	6669	4	US-10-204-708-6 Sequence 6, Appl

28	45.2	2.2	1051	3	US-09-245-041-10 Sequence 10, Appl
29	44.8	2.1	731	1	US-08-451-405A-2 Sequence 2, Appl
30	44.6	2.1	2230	3	US-08-378-313-24 Sequence 24, Appl
31	44.6	2.1	5152	4	US-10-204-708-73 Sequence 73, Appl
32	44.6	2.1	6409	4	US-09-967-908A-1 Sequence 1, Appl
33	44.6	2.1	319608	4	US-09-539-332D-1 Sequence 1, Appl
34	44.6	2.1	319608	4	US-09-679-409-1 Sequence 1, Appl
35	44.4	2.1	1190	4	US-09-350-207-1 Sequence 1, Appl
36	44.4	2.1	2485	4	US-09-889-663A-9 Sequence 9, Appl
37	44.4	2.1	53332	4	US-09-801-861-3 Sequence 64, Appl
38	44.2	2.1	1361	4	US-09-489-847-64 Sequence 64, Appl
39	43.8	2.1	664	4	US-09-904-615-66 Sequence 66, Appl
40	43.8	2.1	2280	3	US-08-813-150-1 Sequence 1, Appl
41	43.8	2.1	2280	4	US-09-546-553-1 Sequence 1, Appl
42	43.6	2.1	2408	4	US-09-594-506-37 Sequence 37, Appl
43	43.4	2.1	1141	4	US-09-800-729-78 Sequence 78, Appl
44	43.4	2.1	3812	4	US-09-784-316-1 Sequence 1, Appl
45	43.4	2.1	5852	1	US-07-867-106-2 Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-482-273-73
Sequence 73, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentm Ver. 2.0
SEQ ID NO 73
LENGTH: 3674
TYPE: DNA
ORGANISM: Homo sapiens
US-09-482-273-73
Query Match 95.8%; Score 2003.8; DB 4; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2034; Conservative 7; Indels 16; Gaps 1;
1 AAGAGACAGCTTTAAGCTTAAATTAAGACGATGTTCAATTTTGTGA 60
1617 AAGAGACAGCTTTAAGCTTAAATTAAGACGATGTTCAATTTTGTGA 1676
61 AAGAGAGTGAATAGCTTCAAGCATGTGAATATCTTCATTTCCCGCC----- 111
1677 AAGAGAGTGAATAGCTTCAAGCATGTGAATATCTTCATTTCCCGCC----- 1736
112 -----CGTTTGTGTTTCTTCAAGTATAGCCTTTAAATGAGAACTAGAG 164
1737 ACACACACACTTTTGTGTTTCTTCAAGTATAGCCTTTAAATGAGAACTAGAG 1796
165 CATTTCAGTACTTGTGTTTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 224
1797 CATTTCAGTACTTGTGTTTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1856
225 TACTTCATACCCCGGTGCTCAATTCCTGCTGATGATGATGATGATGATGATGAT 284
1857 TACTTCATACCCCGGTGCTCAATTCCTGCTGATGATGATGATGATGATGATGAT 1916
```

QY	285	CAAGGCCAAGGAGAACTGGTGAATATAATATTTAATTTTTTTTAACTCTTACAA	344
Db	1917	TCAGTCCCAAGGAACTTGGTAATATAATTTAATTTTTTTTAACTCTTACAA	1976
QY	345	AGCCATGAAATTTATTTGGTGGATGTGCTGTGACAAAGCCATTTCAAATAGATGA	404
Db	1977	AGCCATGAAATTTATTTGGTGGATGTGCTGTGACAAAGCCATTTCAAATAGATGA	2036
QY	405	GCTGTATTTATTTTCCAAAGGTAAATGACATGCAAAAAGTTTCAATAAACTGGGCCA	464
Db	2037	GCTGTATTTATTTTCCAAAGGTAAATGACATGCAAAAAGTTTCAATAAACTGGGCCA	2096
QY	465	TTAACAAATTAATTTAATAACTAAATAGACATCCCTTCTAGTGTTCGCAACCTGCTTA	524
Db	2097	TTAAACAATTAATTAATAACTAAATAGACATCCCTTCTAGTGTTCGCAACCTGCTTA	2156
QY	565	TCCAATTAACAAATTTGAGATCTGTGAAAAAGCTAGTATATTTCAAGAAATGATTTTC	584
Db	2157	TCCAATTAACAAATTTGAGATCTGTGAAAAAGCTAGTATATTTCAAGAAATGATTTTC	2216
QY	585	ATTATTTGAAACGTCTCCCTCTGACGAGCCATTTCCCTTTTCCGGAGTTTACAACT	644
Db	2217	ATTATTTGAAACGTCTCTCCCTCTGACGAGCCATTTCCCTTTTCCGGAGTTTACAACT	2276
QY	645	TTAGAGAGAAATAGTCATGAAAAAGAAAGGAGAAAGGAGAAAGGATTAATAA	704
Db	2277	TTAGAGAGAGAAATAGTCATGAAAAAGAAAGGAGAAAGGAGAAAGGATTAATAA	2336
QY	705	GTAATGCTCAGACCTATGAAAGCTAATCCCTTGGTAAATAATTTAAGACAGCTCAGC	764
Db	2337	GTAATGCTCAGACCTATGAAAGCTAATCCCTTGGTAAATAATTTAAGACAGCTCAGC	2396
QY	765	TTGGTTGAAACAGTATTTTGTTCATCTTCATATTTGACAGAAAGTATTTTCTGACTTGA	824
Db	2397	TTGGTTGAAACAGTATTTTGTTCATCTTCATATTTGACAGAAAGTATTTTCTGACTTGA	2456
QY	885	ATGCAGCTBAGTGTAAAAATTTTATTTTATCATCTTGAAGAAGCTTGAATGAAAAATGA	884
Db	2457	ATGCAGCTBAGTGTAAAAATTTTATTTTATCATCTTGAAGAAGCTTGAATGAAAAATGA	2516
QY	885	TAAATATTGAGGGTTTCCGTGCATATCTGGCTTCATGTGCAAGAAAGCAGAGAAATGA	944
Db	2517	TAAATATTGAGGGTTTCTGTGCATATCTGGCTTCATGTGCAAGAAAGCAGAGAAATGA	2576
QY	945	AAATGTAAATCTTCAACATTCGAAGATCGAAACCCAAAGGGGTAGGCAATCTATGTAGGTT	1004
Db	2577	AAATGTAAATCTTCAACATTCGAAGATCGAAACCCAAAGGGGTAGGCAATCTATGTAGGTT	2636
QY	1005	TTGGAACAAGAGTTTGGTGCACTGTGGTTTATATGCTGGCTCAACCTGCTATTTAACTCTCT	1064
Db	2637	TTGGAACAAGAGTTTGGTGCACTGTGGTTTATATGCTGGCTCAACCTGCTATTTAACTCTCT	2696
QY	1065	GAGCTATATAGTCTTTCATTTCTATTGACAAAGACCTATCGAACACTTGTCTGCAACAGG	1124
Db	2697	GAGCTATATAGTCTTTCATTTCTATTGACAAAGACCTATCGAACACTTGTCTGCAACAGG	2756
QY	1125	CTCTTTATTTAACAATTAGACAGCTACTGTTTGTGTTAAACAACCTTTTCAACCAATATG	1184
Db	2757	CTCTTTATTTAACAATTAGACAGCTACTGTTTGTGTTAAACAACCTTTTCAACCAATATG	2816
QY	1185	TTCTGAGCAAAACGAGACCAATGACTATTTTAAAGAAAGGCTTCCGACATCACTTACAC	1244
Db	2817	TTCTGAGCAAAACGAGACCAATGACTATTTTAAAGAAAGGCTTCCGACATCACTTACAC	2876
QY	1245	ATCCCAAAACTPAAAAAGATCAACTTTCCAACTGAGAAAAGATCTCTGGCTTTGATGGA	1304
Db	2877	ATCCCAAAACTPAAAAAGATCAACTTTCCAACTGAGAAAAGATCTCTGGCTTTGATGGA	2936
QY	1305	AACTTAACGACAGAGTCAACAGGCCACGACCAACAACAACAACAACAACAACAATTGGAA	1364
Db	2937	AACTTAACGACAGAGTCAACAGGCCACGACCAACAACAACAACAACAACAACAATTGGAA	2996
QY	1365	TATTAATCTCAACTCAGCTTTTATATATACATCTTATTAATTTTCTAGTAAAGAAATCAG	1424

Db	2997	TATATTCTCAACTCAGCTTTTAAATAACATCTTATTTTCTCTGAGAGAACTAC	3056
QY	1425	AAATCAGCCTCTTGACATTTATATACAGTTTAAAGCCTCTGCAAGTTACTGTCT	1484
Db	3057	AAATCAGCCTCTTGACATTTATATACAGTTTAAAGCCTCTGCAAGTTACTGTCT	3116
QY	1485	CTCACCGGAGGTATTTTTTTCCTCCCAACCTGGCCCTGTTCCTCCCTCTCTCC	1544
Db	3117	CTCACCGGAGGTATTTTTTTCCTCCCAACCTGGCCCTGTTCCTCCCTCTCTCC	3176
QY	1545	TTTGCAAGAGAAATATTTAACTATTTGGTCCACTCAATATATATTAATATAC	1604
Db	3177	TTTGCAAGAGAAATATTTAACTATTTGGTCCACTCAATATATATTAATATAC	3236
QY	1605	ATTAAAGCATTTAACTTCTCTTTCTAGAAAAATGCAACGGCTAAGCATAGCAAAACA	1664
Db	3237	ATTAAAGCATTTAACTTCTCTTTCTAGAAAAATGCAACGGCTAAGCATAGCAAAACA	3296
QY	1665	AGAGAAATGCTGAGAAATTTGCGCACTGAGACAAGCAATCTGAATAATATTTGCCAAA	1724
Db	3297	AGAGAAATGCTGAGAAATTTGCGCACTGAGACAAGCAATCTGAATAATATTTGCCAAA	3356
QY	1725	GTTCTTTTATATCATATAGTGTACGAAATTTGAAGAGCTATTTTTTTTAATGTCCAA	1784
Db	3357	GTTCTTTTATATCATATAGTGTACGAAATTTGAAGAGCTATTTTTTTTAATGTCCAA	3416
QY	1785	CTAGCACTCATCTCGGAAGACACAGCCAGGAAATGAAGTGAAGTGAAGGTTTATA	1844
Db	3417	CTAGCACTCATCTCGGAAGACACAGCCAGGAAATGAAGTGAAGTGAAGGTTTATA	3476
QY	1845	AATCCATTGTAGCATTTATCCCATATATTTTAAATTCAGAAAAATGTGTTATCTT	1904
Db	3477	AATCCATTGTAGCATTTATCCCATATATTTTAAATTCAGAAAAATGTGTTATCTT	3536
QY	1905	TAGAAATTTGATTCATCATCTTATATGATATGATGATCATGCTCTGGAATAATAAAGC	1964
Db	3537	TAGAAATTTGATTCATCATCTTATATGATATGATGATCATGCTCTGGAATAATAAAGC	3596
QY	1965	ACCAATATGATCTGTATACCAACATACACATATTTATTAATATATATATATCTATATAC	2024
Db	3597	ACCAATATGATCTGTATACCAACATACACATATTTATTAATATATATATCTATATAC	3656
QY	2025	AGCCAAAAAATAAAAA 2041	
Db	3657	AAAAAATAAAAA 3673	
<p>RESULT 2</p> <p>US-09-023-655-341</p> <p>/ Sequence 341, Application US/09023655</p> <p>/ Patent No. 6607879</p> <p>/ GENERAL INFORMATION:</p> <p>/ APPLICANT: Cocks, Benjamin G.</p> <p>/ APPLICANT: Susan G. Stuart</p> <p>/ APPLICANT: Jeffrey J. Seilhamer</p> <p>/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE</p> <p>/ TITLE OF INVENTION: EXPRESSION</p> <p>/ NUMBER OF SEQUENCES: 1508</p> <p>/ CORRESPONDENCE ADDRESS:</p> <p>/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.</p> <p>/ STREET: 3174 PORTER DRIVE</p> <p>/ CITY: PALO ALTO</p> <p>/ STATE: CALIFORNIA</p> <p>/ COUNTRY: USA</p> <p>/ ZIP: 94304</p> <p>/ COMPUTER READABLE FORM:</p> <p>/ MEDIUM TYPE: Floppy disk</p> <p>/ COMPUTER: IBM PC compatible</p> <p>/ OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2</p> <p>/ CURRENT APPLICATION DATA:</p> <p>/ APPLICATION NUMBER: US/09/023.655</p>			

FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 341:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6005 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BEPINOM1
 CLONE: 1432736
 US-09-023-655-341

Query Match 88.6%; Score 1853.4; DB 4; Length 6005;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 2025; Conservative 0; Mismatches 27; Indels 32; Gaps 13;

QY 1 AAGAGACGACTTAACTCCACAGTTTAAAGAGGATGTTCCATGTTTATTGTTA 60
 DB 3911 AAGAGACGACTTAACTCCACAGTTTAAAGAGGATGTTCCATGTTTATTGTTA 3970
 QY 61 AAGAGTGTGATGCTTCAAGCATGATGATTAATCTCCATCTCCCGCC----- 112
 DB 3971 AAGAGTGTGATGCTTCAAGCATGATGATTAATCTCCATCTCCCGCCNNNNNN 4030
 QY 113 -----GCTTTTGTGTTCTTCAAGTACACCTTTTAAATGCAATTAAGTACG 164
 DB 4031 NNNNNNNNNNTTGTCTTCTTCAAGTACACCTTTTAAATGCAATTAAGTACG 4090
 QY 165 CATTTCAGTACTTGTCTTCAATTAAGTACATTAAGTACATTAAGTACATTAAGTAC 224
 DB 4091 CATTTCAGTACTTGTCTTCAATTAAGTACATTAAGTACATTAAGTACATTAAGTAC 4150
 QY 225 TACTCTCCATACCCCGTACTCAATTTCTACTGATGATTAATGATTAAGTACGAT 284
 DB 4151 TACTCTCCATACCCCGTACTCAATTTCTACTGATGATTAATGATTAAGTACGAT 4210
 QY 285 TCAGTCCCAAGAGACATTTGTGAATTAATTTTAA--TTTTTTTTTATCCTTTACA 343
 DB 4211 TCAGTCCCAAGAGACATTTGTGAATTAATTTTAA--TTTTTTTTTATCCTTTACA 4270
 QY 344 AAGCATGATTTTATTTGTTGATGATGCTGTGTACACAAGCATTTCAATAGATG 403
 DB 4271 AAGCATGATTTTATTTGTTGATGATGCTGTGTACACAAGCATTTCAATAGATG 4330
 QY 404 AGCTGTAAATTTTCCAAAGATTAATGATGATCAAAAGTTTCAATTAATAAATG 463
 DB 4331 AGCTGTAAATTTTCCAAAGATTAATGATGATCAAAAGTTTCAATTAATAAATG 4390
 QY 464 AATTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 523
 DB 4391 AATTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4450
 QY 524 ATCCAAATAACAATTTGAAGATGTTGAAAAAGCTAGTTATTTTCAAGAAATGATTT 583
 DB 4451 ATCCAAATAACAATTTGAAGATGTTGAAAAAGCTAGTTATTTTCAAGAAATGATTT 4510
 QY 584 CATTATTTGAACCTGTTCCCTAGAGGCAATTTCCCTTTTCTGAGGATTTAGCAAG 643
 DB 4511 CATTATTTGAACCTGTTCCCTAGAGGCAATTTCCCTTTTCTGAGGATTTAGCAAG 4570
 QY 644 TTATAGAGATAGTCAATGAAAAAGAAAGGAAAGGAGGAAAGGAGGATTAATA 703

DB 4571 TTATAGAGATAGTCAATGAAAAAGAAAGGAAAGGAGGAAAGGAGGATTAATA 4630
 QY 704 AGTAAGTCTGACACTATGAAGCTAATCCCTTTGCTGAATAATTTTAAAGACCTGAG 763
 DB 4631 AGTAAGTCTGACACTATGAAGCTAATCCCTTTGCTGAATAATTTTAAAGACCTGAG 4690
 QY 764 CTGTTGTAAGTAACTGTTTGTGCTATCTCCATATTTGAGAGAGGATTTTCTGACTGC 823
 DB 4691 CTGTTGTAAGTAACTGTTTGTGCTATCTCCATATTTGAGAGAGGATTTTCTGACTGC 4750
 QY 824 AATGAGCTAGATGTAATTTTATTTTATCACTAGAAAGCCTGACTAGAAAAATGA 883
 DB 4751 AATGAGCTAGATGTAATTTTATTTTATCACTAGAAAGCCTGACTAGAAAAATGA 4810
 QY 884 ATAAATATTGAGGGTTTCTGTCATATCTGCTGCTGATGTCGCAAGAAAGCAAGAT-A 942
 DB 4811 ATAAATATTGAGGGTTTCTGTCATATCTGCTGCTGATGTCGCAAGAAAGCAAGAT-A 4870
 QY 943 GAAATGTATCTCCAAATCCAAAGCATGAAACCAAGGGGTAGGCAATTTCTATGAG 1002
 DB 4871 GAAATGTATCTCCAAATCCAAAGCATGAAACCAAGGGGTAGGCAATTTCTATGAG 4930
 QY 1003 TTTTGAACAT-GAAGTTGCTGATCTTGTGTTATGCTGCTCAACTGCTATTAACCTC 1061
 DB 4931 TTTTGAACATGGAAGTTGCTGATCTTGTGTTATGCTGCTCAACTGCTATTAACCTC 4990
 QY 1062 TCTGCTTATGCTCTTCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1121
 DB 4991 TCTGCTTATGCTCTTCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5050
 QY 1122 AGCTCTTATGTAACAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1180
 DB 5051 AGCTCTTATGTAACAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5110
 QY 1181 TAGCTTGAAGCAAG 1240
 DB 5111 GAGCTTGAAGCAAG 5170
 QY 1241 ACACATCCCAAAATCAAAAAGATCAACTCTTCAACTGA--GAAAAGCTCTGCTTTGA 1299
 DB 5171 ACACATCCCAAAATCAAAAAGATCAACTCTTCAACTGAGAAAGAGCTCTGCTTTGA 5230
 QY 1300 ATGG--AACTTACAG 1356
 DB 5231 ATGGAG 5290
 QY 1357 ATTTGAATATTTATTTCAACTCACTCACTTTTAAATTAATTAATTTTCTAGTACA 1416
 DB 5291 ATTTGAATATTTATTTCAACTCACTCACTTTTAAATTAATTAATTTTCTAGTACA 5350
 QY 1417 GAAAGTAAATAGAGCTCTTCAACTTATTAATTAATTAATTAATTAATTAATTAATTA 1475
 DB 5351 GAAAGTAAATAGAGCTCTTCAACTTATTAATTAATTAATTAATTAATTAATTAATTA 5410
 QY 1476 ACTTGTCT-CTCACTGAGAGTA--TTTTTCTCCCACTTGCCTGCTCTCTCTT 1533
 DB 5411 ACTTGTCTCCCACTGAGAGTA--TTTTTCTCCCACTTGCCTGCTCTCTCTCTT 5470
 QY 1534 CC--TCTTCTCTTGGCAAGAGAAATTTTAAATTAATTAATTTTGGGCTCAACTCAATAG 1591
 DB 5471 CCATCTGCTCTCTTGGCAAGAGAAATTTTAAATTAATTTTGGGCTCAACTCAATAG 5530
 QY 1592 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1649
 DB 5531 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5590
 QY 1650 GCATAGCAAAACAAAGAGAAATGCTGA--GAAATTTGCACTGAGACAAGCAATCTGAA 1708
 DB 5591 GCATAGCAAAACAAAGAGAAATGCTGAAGAAATTTGCACTGAGACAAGCAATCTGAA 5650
 QY 1709 TAATATTGCTCCAAAGTCTTTTATATGTCATATAGTGCAGGATTTGAAGGAGCTATT 1768

```
Db 5651 TAAATATTGGCAAAAGTTCTTTTATGTCATATAGTGTCAAGATTTGAGAGACTATT 5710
Qy 1765 TTTTAAATGTTGCAACTGCAACCTCCTTGGGAAGACAGCCAGAGAAATGAGTAG 1828
Db 5711 TTTTAAATGTTGCAACTGCAACCTCCTTGGGAAGACAGCCAGAGAAATGAGTAG 5770
Qy 1828 AAGTGAAGGTTTATTAATCCATTTGTAGCATTTATCCCATATATTTTAAATTCAGAA 1888
Db 5771 AAGTGAAGGTTTATTAATCCATTTGTAGCATTTATCCCATATATTTTAAATTCAGAA 5830
Qy 1888 AAATGTGTTTATCTTAAATTTGTATCAATCTTTATGTAATGTAAGTCAAGCT 1948
Db 5831 AAATGTGTTTATCTTAAATTTGTATCAATCTTTATGTAATGTAAGTCAAGCT 5890
Qy 1948 TCTGATAATTAAGACCAAAATATGATCTGTAACCAATCACACATATTATATTA 2008
Db 5891 TCTGATAATTAAGACCAAAATATGATCTGTAACCAATCACACATATTATTA 5950
Qy 2009 TATATATCTATATTAACAGCCCAAAAAAAAAAGAGAGAGAA 2052
Db 5951 TATATATCTATATTAACAGCCCAAAAAAAAAANNNTAA 5994
```

RESULT 3

```
US-09-439-313-280
; Sequence 280, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-280
```

```
Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

Qy 1 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 60
Db 235 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 294
Qy 61 AAGCAGT 67
Db 295 AAGCAGT 301
```

RESULT 4

```
US-09-352-616A-280
; Sequence 280, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
```

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-280
```

Query Match 3.1%; Score 65.4; DB 4; Length 301;

Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1;

```
Qy 1 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 60
Db 235 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 294
Qy 61 AAGCAGT 67
Db 295 AAGCAGT 301
```

RESULT 5

```
US-09-232-149A-280
; Sequence 280, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-280
```

Query Match 3.1%; Score 65.4; DB 4; Length 301;

Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1;

```
Qy 1 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 60
Db 235 AAGAGACAGACTATTAATCTCCACAGTTAATTAAGACGATGTTCCATGTTTATTTGTA 294
Qy 61 AAGCAGT 67
Db 295 AAGCAGT 301
```

RESULT 6

```
US-09-159-812-280
; Sequence 280, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
```


/ CURRENT FILING DATE: 1998-09-23
/ NUMBER OF SEQ ID NOS: 306
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-159-812-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294
QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 7
US-09-636-215-280
/ Sequence 280, Application US/09636215
/ Patent No. 6620922
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.42717C17
/ CURRENT FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-636-215-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294
QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 8
US-09-685-166a-280
/ Sequence 280, Application US/09685166a

/ Patent No. 6630305
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C21
/ CURRENT FILING DATE: 2000-10-10
/ NUMBER OF SEQ ID NOS: 898
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-685-166a-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294
QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 9
US-09-688-489-280
/ Sequence 280, Application US/09688489
/ Patent No. 6664377
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
/ TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.427D2
/ CURRENT FILING DATE: 2000-10-13
/ NUMBER OF SEQ ID NOS: 338
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-688-489-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294

Page 7

```

:   LENGTH: 1559
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-03-489-847-42

Query Match      2.3%   Score 48.8;   DB 4;   Length 1559;
Best Local Similarity 55.2%   Pred. No. 0.018;
Matches 95;   Conservative 0;   Mismatches 77;   Indels 0;   Gaps 0;

Oy      1893  TGTGTATCATCTTGAAGATTTGTGATTCATAACTTATGTACTATGTGACCTATGCTCTTG 1952
Db      1376  TATGTGTCTTTTTCAGATTACCTCTTAAATTTGATTTATTTTATCATCATGTAAAT 1435
Oy      1953  GATTAATTAAGACCAATATGATTCGTACACCAATCAGACATATTATTTAAATATA 2012

```

LOCATION: (125596)...(128711)
NAME/KEY: exon
LOCATION: (128712)...(128848)
NAME/KEY: intron
LOCATION: (128849)...(133400)
NAME/KEY: exon
LOCATION: (133401)...(133469)
NAME/KEY: intron
LOCATION: (133470)...(134652)
NAME/KEY: exon
LOCATION: (134653)...(134773)
NAME/KEY: intron
LOCATION: (134774)...(136116)
NAME/KEY: exon
LOCATION: (136117)...(136261)
NAME/KEY: intron
LOCATION: (136262)...(137936)
NAME/KEY: exon
LOCATION: (137937)...(138053)
NAME/KEY: intron
LOCATION: (138054)...(138637)
NAME/KEY: exon
LOCATION: (138638)...(138766)
NAME/KEY: intron
LOCATION: (138767)...(138864)
NAME/KEY: exon
LOCATION: (138865)...(138940)
NAME/KEY: intron
LOCATION: (138941)...(139765)
NAME/KEY: exon
LOCATION: (139766)...(139860)
NAME/KEY: intron
LOCATION: (139861)...(142245)
NAME/KEY: exon
LOCATION: (142246)...(142445)
NAME/KEY: intron
LOCATION: (142446)...(143605)
NAME/KEY: exon
LOCATION: (143606)...(143738)
NAME/KEY: intron
LOCATION: (143739)...(145838)
NAME/KEY: exon
LOCATION: (145839)...(145931)
NAME/KEY: intron
LOCATION: (145932)...(147385)
NAME/KEY: exon
LOCATION: (147386)...(147544)
NAME/KEY: intron
LOCATION: (147545)...(153274)
NAME/KEY: exon
LOCATION: (153275)...(153321)
NAME/KEY: intron
LOCATION: (153322)...(155088)
NAME/KEY: exon
LOCATION: (155089)...(155231)
NAME/KEY: intron
LOCATION: (155232)...(156025)
NAME/KEY: exon
LOCATION: (156026)...(156151)
NAME/KEY: intron
LOCATION: (156152)...(156826)
NAME/KEY: exon
LOCATION: (156827)...(156928)
NAME/KEY: intron
LOCATION: (156929)...(163399)
NAME/KEY: exon
LOCATION: (163400)...(163586)
US-09-676-610B-24

Query Match 2.3%; Score 48.4; DB 4; Length 169998;
Best Local Similarity 55.9%; Pred. No. 0.15;
Matches 113; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

QY 1869 ATATATTTTAAATTCAGAAAATGCTGTATTCCTTAGAATTTGTATCAATACTTTA 1928
|||
Db 158916 ATATATATGATATATATTTTAGAGATATATTTTAGAGATATATTTTAGAGATTTA 158975
QY 1929 TGTACTATGTGACTCATGCTTCTGATTAATAAGACCAATATGTATCTGTAAACACA 1968
|||
Db 158976 TATATATTTT--ATATATATTTAGAGATATATATCTCTAAATATATATCTCTCTTAA 159032
QY 1989 ATCACACATATATATTTAAATATATATCTATATTAACAGCCAAAATTTTAAAGAGAGA 2048
|||
Db 159033 TATATATATATCTCTCTCTCTAAATATATATATATATATATATATATATATATATATAT 159032
QY 2049 AGAAAAAGAAAGAGAGAGGGGG 2070
|||
Db 159093 AATAAAAAGAAAGCTCAGTTGG 159114

RESULT 15
US-09-877-177A-10
; Sequence 10, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HBR2-Neu Gene Expression
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-10

Query Match 2.3%; Score 48.4; DB 4; Length 197496;
Best Local Similarity 55.9%; Pred. No. 0.16;
Matches 113; Conservative 0; Mismatches 86; Indels 3; Gaps 1;
QY 1869 ATATATTTTAAATTCAGAAAATGCTGTATTCCTTAGAATTTGTATCAATACTTTA 1928
|||
Db 166916 ATATATATGATATATATTTAGAGATATATATTTAGAGATATATATTTAGAGATTTA 166975
QY 1929 TGTACTATGTGACTCATGCTTCTGATTAATAAGACCAATATGTATCTGTAAACACA 1968
|||
Db 166976 TATATATTTT--ATATATATTTAGAGATATATATCTCTAAATATATATCTCTCTTAA 167032
QY 1989 ATCACACATATATATTTAAATATATATCTATATTAACAGCCAAAATTTTAAAGAGAGA 2048
|||
Db 167033 TATATATATATCTCTCTCTCTAAATATATATATATATATATATATATATATATATATAT 167092
QY 2049 AGAAAAAGAAAGAGAGGGGG 2070
|||
Db 167093 AATAAAAAGAAAGCTCAGTTGG 167114

Search completed: May 6, 2004, 00:57:04
Job time: 161 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 12:47:03 ; Search time 816 Seconds
(without alignments)

10886.008 Million cell updates/sec

Title: US-09-646-569A-60
Perfect score: 2091
Sequence: 1 aagaagacagactactactc.....ggaagagaagggggggaggt 2091

Scoring table: IDENTITY NUC
Gapop 10.0, Gapept 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2091	100.0	2091	AA233595	AA233595 Human bre
2	2003.8	95.8	3674	AA298079	AA298079 Human sec
3	2003.8	95.8	3674	AA211692	AA211692 Human sec
4	2003.8	95.8	3674	ABK69788	ABK69788 Human sec
5	2000.4	95.7	10427	ABK69943	ABK69943 Human sec
6	1878.6	89.8	1909	AB192123	AB192123 Human Tum
7	1878.6	89.8	1909	ABX72048	ABX72048 DNA encod
8	1366.6	65.4	3461	ABY25337	ABY25337 Human pro
9	591.4	28.3	594	ABT10123	ABT10123 Human bre
10	425.8	20.4	488	ABX74748	ABX74748 Human cDN
11	331	15.8	331	AB162296	AB162296 Colon adn
12	331	15.8	331	AB166826	AB166826 Lung canc
13	331	15.8	331	ABN94862	ABN94862 Gene #136
14	307.4	14.7	472	ABR09999	ABR09999 Human bre
15	194.2	9.3	1584	AA283630	AA283630 DNA encod
16	136	6.3	140	AA212827	AA212827 Human sec
17	95.2	4.6	547	ABK62858	ABK62858 Rat seque
18	95.2	4.6	547	ABK62857	ABK62857 Toxicity-
19	65.4	3.1	301	AA06513	AA06513 Human imm
20	65.4	3.1	301	AAH93629	AAH93629 Human pro
21	65.4	3.1	301	AA563721	AA563721 Human pro
22	65.4	3.1	301	AAH02594	AAH02594 Prostate
23	65.4	3.1	301	AAH84943	AAH84943 Human pro

ALIGNMENTS

24	65.4	3.1	301	5	ACA59530	ACA59530 Prostate
25	65.4	3.1	301	6	ABL95093	ABL95093 Human Jp8
26	65.4	3.1	301	7	ACC95257	ACC95257 Prostate
27	65.4	3.1	301	7	ADB13730	ADB13730 Human pro
28	60	2.9	60	6	ABN44057	ABN44057 Human spl
29	58.6	2.8	5102	6	ABL92274	ABL92274 Chemical1
30	58	2.8	19653	6	ABL33334	ABL33334 Human imm
31	58	2.8	20420	6	AAK73165	AAK73165 Human imm
32	58	2.8	20420	6	ABK69933	ABK69933 Human sec
33	56.4	2.7	7351	6	AB132028	AB132028 Human imm
34	56.4	2.7	10329	6	AB134123	AB134123 Human imm
35	55.8	2.7	390	7	ABX36811	ABX36811 Bovine ES
36	55.6	2.7	1994	5	AAH48294	AAH48294 Honeybee
37	55	2.6	1676	4	AAH72649	AAH72649 Human cer
38	55	2.6	1702	5	ABV27467	ABV27467 Human pro
39	55	2.6	1702	5	ABV27724	ABV27724 Human pro
40	55	2.6	1702	5	ABV25281	ABV25281 Human pro
41	55	2.6	1702	5	ABV21893	ABV21893 Human pro
42	54.8	2.6	267	4	AAH43643	AAH43643 SSG #9.1
43	54.8	2.6	389	4	AA186169	AA186169 Human pol
44	54.6	2.6	1501	7	AB210188	AB210188 Haematopo
45	54.6	2.6	1501	9	ADB84162	ADB84162 Human lym

RESULT 1
ID AA233595 standard; cDNA; 2091 BP.
AC AA233595;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human breast tumour-associated EST 55.

KW Expressed sequence tag; EST; human; breast; cancer; cytostatic;
KW medicaments; gene therapy; treatment; fat metabolism; ss.

OS Homo sapiens.
XX
XX DB19813835-A1.
XX
PD 23-SEP-1999.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX 20-MAR-1998; 98DE-01013835.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX WPI; 1999-528979/45.
XX P-PSDB; AAY48516.
XX Human nucleic acid sequences and protein products from normal breast
PT tissue, useful for breast cancer therapy.
PT
PS Claim 1a; 142-143; 206pp; German.

XX This invention describes novel human nucleic acid sequences from normal
XX breast tissue which have cytosstatic activity. The nucleic acid sequences
XX can be used to produce and isolate full-length gene sequences. They can
XX be used to express proteins, which can be used as tools to find an
XX activity against breast cancer. The sequences can be used in sense or
XX antisense form. They are especially useful for medicaments for gene
XX therapy to treat breast cancer and for treating illnesses associated with
XX fat metabolism. AA233541-Z13610 represent expressed sequence tags
XX described in the method of the invention

Sequence 2091 BP; 702 A; 375 C; 364 G; 650 T; 0 U; 0 Other;

Query Match 100.0%; Score 2091; DB 2; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGACAGACTTAACTCCACAGTTAATTAGACGATGTCATGTTATTTGTTA 60
DB 1 AAGAGACAGACTTAACTCCACAGTTAATTAGACGATGTCATGTTATTTGTTA 60
QY 61 AAGCAGTGTGAATAGCCTTCAAGCATGTGAATATCTTCCCTCCGCGCTTTTG 120
DB 61 AAGCAGTGTGAATAGCCTTCAAGCATGTGAATATCTTCCCTCCGCGCTTTTG 120
QY 121 TTTCTTTCAGTAGACACCTTTTAAATGACAGATCTAGAGGATTCAGTAATTG 180
DB 121 TTTCTTTCAGTAGACACCTTTTAAATGACAGATCTAGAGGATTCAGTAATTG 180
QY 181 CTTCGAATCAATTAAGTCAAAATGTATGAAAATTTTGTGCTTCTCATACCCG 240
DB 181 CTTCGAATCAATTAAGTCAAAATGTATGAAAATTTTGTGCTTCTCATACCCG 240
QY 241 TGTACTCAAAATCTCTACTGTATGAATTAATGCTTAAGTAATTCAGTGCAGAGAA 300
DB 241 TGTACTCAAAATCTCTACTGTATGAATTAATGCTTAAGTAATTCAGTGCAGAGAA 300
QY 301 CTGTGTGAATTAATTAATTTTATTTTATCTTTACAAAGCCATGATTTTAT 360
DB 301 CTGTGTGAATTAATTAATTTTATTTTATCTTTTATCTTTACAAAGCCATGATTTAT 360
QY 361 TGGTGTATGTGTCTCTGACCAAGCATTTCAATAGATGAGCTGTAAATTTTC 420
DB 361 TGGTGTATGTGTCTCTGACCAAGCATTTCAATAGATGAGCTGTAAATTTTC 420
QY 421 CAAAGATATGACATGCAAAAGTTCAATAAACTGGCCATTAACAATAATTA 480
DB 421 CAAAGATATGACATGCAAAAGTTCAATAAACTGGCCATTAACAATAATTA 480
QY 481 TAACTAATAGATTCCTTTCTAGTTTTTCCAACTGCTATCCATAACAATTG 540
DB 481 TAACTAATAGATTCCTTTCTAGTTTTTCCAACTGCTATCCATAACAATTG 540
QY 541 AAGATCGTGAAGAAAGCTATTAATTTGAGAAATGATTTTCAATTAAGAACTGTC 600
DB 541 AAGATCGTGAAGAAAGCTATTAATTTGAGAAATGATTTTCAATTAAGAACTGTC 600
QY 601 TCCCTAGCAGGCAATTTTCCCTTTTCCGGAAGTTTAGCAAGTTTAGAGAAATAGTC 660
DB 601 TCCCTAGCAGGCAATTTTCCCTTTTCCGGAAGTTTAGCAAGTTTAGAGAAATAGTC 660
QY 661 AAGAAAAGAAAGGAAAGGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 661 AAGAAAAGAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 ATGAAGCTAATCCCTTTGCTAGAAATATTTAAGACAGCTCAGCTGTGTAAGT 780
DB 721 ATGAAGCTAATCCCTTTGCTAGAAATATTTAAGACAGCTCAGCTGTGTAAGT 780
QY 781 TTTGTATCTTCCATATTTGACGAGAGGATTTTCTGACTTGAAGTGAAGTGA 840
DB 781 TTTGTATCTTCCATATTTGACGAGAGGATTTTCTGACTTGAAGTGAAGTGA 840
QY 841 AATTTTATTTTATCTAGTCTAGAAAGCTTGAAGTGAAGTGAAGTGAAGTGA 900
DB 841 AATTTTATTTTATCTAGTCTAGAAAGCTTGAAGTGAAGTGAAGTGAAGTGA 900
QY 901 CCTGTCTATCTGTGCTGATGTCAGAAAGCAGAAATGAAAATGTAATCTCCAC 960
DB 901 CCTGTCTATCTGTGCTGATGTCAGAAAGCAGAAATGAAAATGTAATCTCCAC 960
QY 961 ATCCAAAGCATGCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 961 ATCCAAAGCATGCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020

QY 1021 GTGCATCTTGTGTTTANGCTGCTCACTGCTATTAACCTCTGCTTATAGTCTTTC 1080
DB 1021 GTGCATCTTGTGTTTANGCTGCTCACTGCTATTAACCTCTGCTTATAGTCTTTC 1080
QY 1081 ATTCTATTAGACAAGACGATGCAACACTTGTCTGCAAGAGCTCTTTAGTTAACAT 1140
DB 1081 ATTCTATTAGACAAGACGATGCAACACTTGTCTGCAAGAGCTCTTTAGTTAACAT 1140
QY 1141 TTAGCAGCTACTGTGTGTGTTAAACACTTTTCAACCAATAGTCTGAGGAAAGCG 1200
DB 1141 TTAGCAGCTACTGTGTGTGTTAAACACTTTTCAACCAATAGTCTGAGGAAAGCG 1200
QY 1201 AGCAATGACTATTTAAGAAAGGCTTCCAGCATCTTACATCCCAAACTAATAA 1260
DB 1201 AGCAATGACTATTTAAGAAAGGCTTCCAGCATCTTACATCCCAAACTAATAA 1260
QY 1261 GATCAACTCTTCCACTGAGAAAGACTCTGCTTTGAATGAAATTTACAGCAGAG 1320
DB 1261 GATCAACTCTTCCACTGAGAAAGACTCTGCTTTGAATGAAATTTACAGCAGAG 1320
QY 1321 TCAAGGCCAGGCAACAACAAGCAACAAACAAATTTGAAATGAAATGAAATGAA 1380
DB 1321 TCAAGGCCAGGCAACAACAAGCAACAAACAAATTTGAAATGAAATGAAATGAA 1380
QY 1381 CGTTTAAATATACATCTTATTTTCTGATGAGAAATCAATGAGCTCTTCA 1440
DB 1381 CGTTTAAATATACATCTTATTTTCTGATGAGAAATCAATGAGCTCTTCA 1440
QY 1441 CATTTATATACATTTAATAGCTCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CATTTATATACATTTAATAGCTCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 TTTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 TTTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 TTTAACAATTTGGGTCCTCACTCAATTAATTAATTAATTAATTAATTAATTAAT 1620
DB 1561 TTTAACAATTTGGGTCCTCACTCAATTAATTAATTAATTAATTAATTAATTAAT 1620
QY 1621 TTTCTTTTCAAGAAATGCAAGGCTAAGGCAAGCAAAACAAAGAAATGCTAGAA 1680
DB 1621 TTTCTTTTCAAGAAATGCAAGGCTAAGGCAAGCAAAACAAAGAAATGCTAGAA 1680
QY 1681 ATTGCGCATGGAACAAGCAATCTGAATTAATTTGGCAAAAGTCTTTTATGTCAT 1740
DB 1681 ATTGCGCATGGAACAAGCAATCTGAATTAATTTGGCAAAAGTCTTTTATGTCAT 1740
QY 1741 ATAGTGTAGAGATTTGAAGAGCTATTTTATTTTATGTTGCACTAGCACTCATCTTC 1800
DB 1741 ATAGTGTAGAGATTTGAAGAGCTATTTTATTTTATGTTGCACTAGCACTCATCTTC 1800
QY 1801 GGAAGCAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
DB 1801 GGAAGCAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
QY 1861 TTTATCCATATATTTTAAATTTCAAGAAATTTGTTATCTTGAATTTTGTATTTCA 1920
DB 1861 TTTATCCATATATTTTAAATTTCAAGAAATTTGTTATCTTGAATTTTGTATTTCA 1920
QY 1921 ATACTTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
DB 1921 ATACTTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 TAAACCAATCAACATATTTATTTAATTAATTAATTAATTAATTAATTAATTAAT 2040
DB 1981 TAAACCAATCAACATATTTATTTAATTAATTAATTAATTAATTAATTAATTAAT 2040
QY 2041 AGAAG 2091
DB 2041 AGAAG 2091

RESULT 2
AAZ98079
ID AAZ98079 standard; cDNA; 3674 BP.
AC AAZ98079;
DT 09-MAY-2000 (first entry)
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:73.
KM Human; secreted protein; diagnosis; cyostatic; immunosuppressive; KM antiinflammatory; nocitropic; neuroprotective; antiallergic; cancer; KM tumour; neurodegenerative disorder; developmental abnormality; allergy; KM foetal deficiency; blood disorders; immune system disorder; arthritis; KM autoimmune disease; hepatic disease; renal disease; inflammation; KM Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; KM infection; AIDS; spinal cord injury; transplant rejection; diabetes; KM asthma; sepsis; acne; psoriasis; cardiovascular disorder; KM reproductive disorder; gastrointestinal disorder; respiratory disorder; KM metabolic disorder; food additive; preservative; ss.
OS Homo sapiens.
PN MO200004140-A1.
PD 27-JAN-2000.
PX 14-JUL-1999; 99MO-US015849.
PR 15-JUL-1998; 98US-00929212. PR 15-JUL-1998; 98US-00929222. PR 15-JUL-1998; 98US-00929565.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y, PE, PI Lafleur DW, Ehner R, Olsen HS, Brewer LA, Florence KA, Young J; PI PI Mucenski M, Endress GA, Soppet DR; XX
DR WPI: 2000-161128/14. P-PsDB; AA87126.
XX New isolated human genes, useful for diagnosis and treatment of, e.g. PT cancers, neurological or blood disorders.
PS Claim 1; Page 348-349; 494pp; English.
XX The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the CC human secreted proteins given in AA87064 to AA87123. Human secreted CC protein can have activities based on the tissues and cells the genes are CC expressed in. Examples of activities include: cyostatic; CC immunosuppressive; antiinflammatory; nocitropic; neuroprotective; and CC antiallergic. The polynucleotides and their corresponding secreted CC polypeptides are useful for preventing, treating or ameliorating medical CC conditions, e.g. by protein or gene therapy. Also pathological conditions CC can be diagnosed by determining the presence of mutations in the new CC sample or by determining the presence of mutations in the new CC polynucleotides. Human secreted proteins and their polynucleotides can CC be used for developing products for the diagnosis or treatment of cancer, CC tumours, neurodegenerative disorders, developmental abnormalities and CC foetal deficiencies, blood disorders, diseases of the immune system, CC autoimmune diseases, hepatic and renal disease, inflammation, allergies, CC Alzheimer's disease, behavioural disorders, schizophrenia, osteoporosis, CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection, CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, CC reproductive disorders, gastrointestinal disorders, respiratory disorders CC and metabolic disorders. The proteins or polynucleotides can also be used CC as food additives or preservatives. The proteins are also useful for CC identifying their binding partners. AAZ98008 to AAZ98016 and AA87063 are CC sequence used in the exemplification of the present invention XX
Sequence 3674 BP; 1221 A; 670 C; 624 G; 1159 T; 0 U; 0 Other;

[illegible]

Db 2637 TTGGAGCATGAAGTTGGTGCATCTTGTTTATGCTGGCTCAAGCTGATTAATTAACCTCTCT
 QY 1065 GGGTTATAGTCTCTTCATTCTATTAGACAAGACGATGCAACACTTGCTGGACAAG 1124
 Db 2697 GGGTTATAGTCTCTTCATTCTATTAGACAAGACGATGCAACACTTGCTGGACAAG 2756
 QY 1125 CTCTTATAGTAAACAATTTAGACACTCTGTTGTGTTAAACACACTTTTCCACCAATAG 1184
 Db 2757 CTCTTATAGTAAACAATTTAGACACTCTGTTGTGTTAAACACACTTTTCCACCAATAG 2816
 QY 1185 TTCTGAGGCAACGAGAGCAATGACTATTATTAAGAAAGCTTTCCAGCATCACTTAAC 1244
 Db 2817 TTCTGAGGCAACGAGAGCAATGACTATTATTAAGAAAGCTTTCCAGCATCACTTAAC 2876
 QY 1245 ATCCCAAAACTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCTTTGAATGA 1304
 Db 2877 ATCCCAAAACTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCTTTGAATGA 2936
 QY 1305 AACTACAGCAGAGATCAACAGGCCACGCAACCAACAACAACCAACCAATTTGGA 1364
 Db 2937 AACTACAGCAGAGATCAACAGGCCACGCAACCAACAACAACAACCAATTTGGA 2996
 QY 1365 TATTATTCTCACTCAAGCTTTATTAATATACATCTTAATTTTCTAGTAGAAGAACTAC 1424
 Db 2997 TATTATTCTCACTCAAGCTTTATTAATATACATCTTAATTTTCTAGTAGAAGAACTAC 3056
 QY 1425 AATTCAGCCCTCTCAACATTTATATACAGTTTAATAGCCTCTGCAAGTCTTCT 1484
 Db 3057 AATTCAGCCCTCTCAACATTTATATACAGTTTAATAGCCTCTGCAAGTCTTCT 3116
 QY 1485 CTCACCTGAGATATTTTCTCTCCACCTGCTGCTGCTCTCTCTCTCTCTCTCTCT 1544
 Db 3117 CTCACCTGAGATATTTTCTCTCCACCTGCTGCTGCTGCTCTCTCTCTCTCTCTCT 3176
 QY 1545 TTTCGAAAGGAAATTTTAACAATTTGGGTCCAACTCAATTAATTAATTAATTAATAC 1604
 Db 3177 TTTCGAAAGGAAATTTTAACAATTTGGGTCCAACTCAATTAATTAATTAATTAATAC 3236
 QY 1605 ATTAAAGCATTTTACTCTCTCTCTAGAAAAATGCAAGGCTAAGCATAGACAACAA 1664
 Db 3237 ATTAAAGCATTTTACTCTCTCTCTAGAAAAATGCAAGGCTAAGCATAGACAACAA 3296
 QY 1665 AGGAAATGCTGGAATTTGCACTGAGACAAGAACTCAATTAATTAATTTGGCAAA 1724
 Db 3297 AGGAAATGCTGGAATTTGCACTGAGACAAGAACTCAATTAATTAATTTGGCAAA 3356
 QY 1725 GTTCTTTTATGTCATATAGTGTCAAGATTTGAGAGGCTATTTTATTTATTTGCA 1784
 Db 3357 GTTCTTTTATGTCATATAGTGTCAAGATTTGAGAGGCTATTTTATTTATTTGCA 3416
 QY 1785 CTGCAACTCATCTTGGAGAGACACGCGAGAAATGAAGTGAAGTGAAGGTTTATA 1844
 Db 3417 CTGCAACTCATCTTGGAGAGACACGCGAGAAATGAAGTGAAGTGAAGGTTTATA 3476
 QY 1845 AATTCATTTGTAAGATTTATCCCATATATTTTAAATTAAGAAAAATGTTTATCTT 1904
 Db 3477 AATTCATTTGTAAGATTTATCCCATATATTTTAAATTAAGAAAAATGTTTATCTT 3536
 QY 1905 TAGAATTTGTATCAACTTATATGTAATGTAAGTCAATGCTTGTGATTAATTAAGC 1964
 Db 3537 TAGAATTTGTATCAACTTATATGTAATGTAAGTCAATGCTTGTGATTAATTAAGC 3596
 QY 1965 ACAAAATATGATCTGTAACCAACATCAACATATATTAATTAATTAATTAATTAAC 2024
 Db 3597 ACAAAATATGATCTGTAACCAACATCAACATATATTAATTAATTAATTAATTAAC 3656
 QY 2025 AGCCAAAAA 2041
 Db 3657 AAAAAA 3673

RESULT 3

AAD11692
 ID AAD11692 standard; cDNA; 3674 BP.
 AC AAD11692;
 XX 24-SEP-2001 (first entry)
 DE Human secreted protein-encoding gene 63 cDNA clone HUVE077, SRQ ID NO:73.
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; hematopoietic disorder;
 KW immune system disease; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KW cell culture; Chemotaxis; vulnirary; binding partner identification;
 KW gene therapy; ss.
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 55..198
 FT /*tag= a
 FT /product= "Human secreted protein precursor"
 FT 55..135
 FT /*tag= b
 FT mat_peptide
 FT 135..195
 FT /*tag= c
 FT /product= "Mature human secreted protein"
 FT
 PN WO200151504-A1.
 PD 19-JUL-2001.
 PE 12-JAN-2001; 2001MO-US000911.
 XX 13-JAN-2000; 2000US-00482273.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Komatsu-Lie GA, Duan DR, Rosen CA, Moore PA, Shi Y;
 PI Laflair DW, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;
 PI Endress GA, Muscenski M, Edner R;
 XX WPI; 2001-425865/45.
 DR P-PSDB; AAE06103.
 PT Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PS Claim 1; Page 715-716; 864pp; English.
 CC AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
 CC protein genes, and AAE06041-AAE06132 represent the proteins they encode.
 CC AAE06133-AAE06205 represent human secreted protein fragments. The
 CC secreted proteins and their genes are useful for preventing, treating or
 CC ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 71 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiotensin disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell

Dd	3537 TAGAATTTCGATTAACACTTAACTTAAGTACTAGTCACTCAGCCAGCTCTCGATTAATAAAGC	3596
Oy	1965 ACCAAATATGTATCTGTGAACCAATCACACATATTATTTAAATATATCTATATTAAC	2022
Dd	3597 ACCAAATATGTATCTGTGAACCAATCACACATATTATTTAAATATATCTATATTAAC	3658
Oy	2025 AGCCCCAAAAAAA 2041	
Dd	3657 AAAAAAAAAAAAAAAA 3673	
<hr/>		
RESULT 4		
ABK69788		
ID	ABK69788 standard; cDNA; 3674 BP.	
XX	ABK69788;	
XX		
Dt	15-JUL-2002 (first entry)	
XX		
DE	Human secreted protein gene 63.	
XX		
KM	Human; ss; gene; secreted protein; gene therapy; immunosuppressive;	
KM	antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;	
KM	vaccitropic; cerebroprotective; nootropic; neuroprotective; antibacterial;	
KM	vinciclovir; fungicide; ophthalmological; autoimmune disease; neoplasm;	
KM	rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;	
KM	cardiovascular disorder; cerebrovascular disorder; cerebral ischemia;	
KM	angiogenesis; nervous system disorder; Alzheimer's disease; infection;	
KM	ocular disorder; corneal infection; wound healing; skin aging;	
KM	epithelial cell proliferation; food additive.	
OS	Homo sapiens.	
PN	WO200226931-A2.	
XX		
XX	04-APR-2002.	
PD		
XX	24-SEP-2001; 2001WO-US029871.	
PF		
PR	25-SEP-2000; 2000US-0234925P.	
XX	12-JAN-2001; 2001WO-US000911.	
EA	(HUMAN-) HUMAN GENOME SCI INC.	
PI	Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y,	
PI	Lafleur DW, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;	
PI	Address GA, Mucenski M, Edner R;	
XX		
DR	WPI, 2002-362489/39.	
XX	F-PSTDB; ABG33925.	
PT		
PT	Novel 71 isolated secreted polypeptides and polynucleotides encoding the	
PT	polypeptides, useful for treating Huntington's disease, sepsis,	
PT	meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,	
XX	asthma.	
XX		
XX	Claim 1; Page 1197-1198; 1478bp; English.	
CC	The invention relates to an isolated nucleic acid molecule (or its	
CC	fragment, homologous complement or allelic variant) encoding a human	
CC	secreted protein (and its fragment, domain, epitope, variant, secreted	
CC	form and species variant). Also included are a recombinant vector	
CC	comprising the nucleic acid, a recombinant host cell comprising the	
CC	vector, an antibody against the secreted protein, a recombinant host cell	
CC	that expresses the secreted protein and a method of identifying a binding	
CC	partner of the secreted protein. The nucleic acid and protein are used to	
CC	prevent, diagnose, treat or ameliorate a medical condition in e.g.	
CC	humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for	
CC	example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative	
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders	
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,	
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,	

Query	Best Local Match	Similarity	Score	DB	Length	Matches	Mismatches	Indels	Gaps
QY	1	AAGAGACGAGTAACTTAATCCACAGTAAATTAAGACGATATGTCATGTTATTTGTA	95.8%	2003.8	3674	60	0	0	0
Db	1617	AAGAGACGAGTAACTTAATCCACAGTAAATTAAGACGATATGTCATGTTATTTGTA	98.9%	2003.8	3674	1676	0	0	0
QY	61	AAGCAGTGTGAAAGACCTTCAAGCATGTGAATATCTTCATCTTCCCGC-----	95.8%	2003.8	3674	111	0	0	0
Db	1677	AAGCAGTGTGAAAGACCTTCAAGCATGTGAATATCTTCATCTTCCCGC-----	98.9%	2003.8	3674	1736	0	0	0
QY	112	-----CGCTTTGTTTCCTTCAGGTAGACACCTTTAAATGACGAATCACTAGG	95.8%	2003.8	3674	164	0	0	0
Db	1737	ACACACACACTTTGTTTCCTTCAGGTAGACACCTTTAAATGACGAATCACTAGG	98.9%	2003.8	3674	1796	0	0	0
QY	165	CATTTCAGTAACTTGTCTTCAATCAATTAAGTCAATGTATGAAACATTTTGTGCC	95.8%	2003.8	3674	224	0	0	0
Db	1797	CATTTCAGTAACTTGTCTTCAATCAATTAAGTCAATGTATGAAACATTTTGTGCC	98.9%	2003.8	3674	1856	0	0	0
QY	225	TACTCTCATACCCCGGTACTCAAAATCTCTCACTGATGAATATGCTTAAGATGAT	95.8%	2003.8	3674	284	0	0	0
Db	1857	TACTCTCATACCCCGGTACTCAAAATCTCTCACTGATGAATATGCTTAAGATGAT	98.9%	2003.8	3674	1916	0	0	0
QY	285	TCAGTGCACAAAGAGACTGTGTGAATTAATTTATTTTTTTTATCTTTACAA	95.8%	2003.8	3674	344	0	0	0
Db	1917	TCAGTGCACAAAGAGACTGTGTGAATTAATTTATTTTTTTTATCTTTACAA	98.9%	2003.8	3674	1976	0	0	0
QY	345	AGCCATGGATTTTATTTGGTGTGATGTGTCTGTGACAAAGCCATTTCAATAGATGA	95.8%	2003.8	3674	404	0	0	0
Db	1977	AGCCATGGATTTTATTTGGTGTGATGTGTCTGTGACAAAGCCATTTCAATAGATGA	98.9%	2003.8	3674	2038	0	0	0
QY	405	GCTGTTATTTATTTCCAAAGAGTATGACATGCAAAAGTTTCAATAAATCTGGGCCA	95.8%	2003.8	3674	464	0	0	0
Db	2037	GCTGTTATTTATTTCCAAAGAGTATGACATGCAAAAGTTTCAATAAATCTGGGCCA	98.9%	2003.8	3674	2096	0	0	0
QY	465	TTAACAAATAATTATTAACATAATTAAGCATTTCCCTTGTAGTTTTCCTGCTCTA	95.8%	2003.8	3674	524	0	0	0
Db	2097	TTAACAAATAATTATTAACATAATTAAGCATTTCCCTTGTAGTTTTCCTGCTCTA	98.9%	2003.8	3674	215	0	0	0
QY	525	TCCATTAACAATTTGAGATTCGTGAAAAAGCTGATATTTTCAAGAAATGATTTTC	95.8%	2003.8	3674	584	0	0	0
Db	2157	TCCATTAACAATTTGAGATTCGTGAAAAAGCTGATATTTTCAAGAAATGATTTTC	98.9%	2003.8	3674	221	0	0	0
QY	585	ATTATTTGAAAGCTGTTCCCTCCTAGAGGACATTTTCCCTTTTCTGGAGTTTACAACT	95.8%	2003.8	3674	644	0	0	0
Db	2217	ATTATTTGAAAGCTGTTCCCTCCTAGAGGACATTTTCCCTTTTCTGGAGTTTACAACT	98.9%	2003.8	3674	227	0	0	0
QY	645	TTAGAGAGATATGATGAAAAAGAAAGGAGAAAGGAGAAAGGATTAATAA	95.8%	2003.8	3674	704	0	0	0
Db	2277	TTAGAGAGAGATATGATGAAAAAGAAAGGAGAAAGGAGAAAGGATTAATAA	98.9%	2003.8	3674	233	0	0	0
QY	705	GTAAGAGCTCAACCTATGAAAGTATCCCTTGTAGAAATATTTTAAAGCAGCTCAGC	95.8%	2003.8	3674	764	0	0	0
Db	2337	GTAAGAGCTCAACCTATGAAAGTATCCCTTGTAGAAATATTTTAAAGCAGCTCAGC	98.9%	2003.8	3674	2396	0	0	0
QY	765	TTGGTTGAAAGTGAAGTTTGTATCTTCATATTTTGACAGAAAGTATTTCTGACTTGA	95.8%	2003.8	3674	824	0	0	0
Db	2397	TTGGTTGAAAGTGAAGTTTGTATCTTCATATTTTGACAGAAAGTATTTCTGACTTGA	98.9%	2003.8	3674	245	0	0	0
QY	825	ATGACGCTAGATGTAATTTTATTTTATTCATCTAGAAAGCCTGACTAGAAAAATGAA	95.8%	2003.8	3674	884	0	0	0

```

Db      2457 ATGAGCTAGATGAAATTTTATTTATCATCTGAGAAAGCCTTGACTGAGAAATGAA 2516
Qy      885 TAAATATTTGAGGGTTTCTGTCATATCTGCTTGACATGTCAGAAAGAGAAATAG 944
Db      2517 TAAATATTTGAGGGTTTCTGTCATATCTGCTTGACATGTCAGAAAGAGAAATAG 2576
Qy      945 AAATGATATCTCCAACTCCAGAGATGAAACCCAGGGGTAGGCAATTTATGTAGT 1004
Db      2577 AAATGATATCTCCAACTCCAGAGATGAAACCCAGGGGTAGGCAATTTATGTAGT 2636
Qy      1005 TTGACATGAGATTTGGTGCATCTTGGTTATGCTGGCTCACTGATTAACCTCTCT 1064
Db      2637 TTGACATGAGATTTGGTGCATCTTGGTTATGCTGGCTCACTGATTAACCTCTCT 2696
Qy      1065 GGGTTATAGTCTCTTCACTTCTATTGACAAAGACAGTTCGACACTTGTCCGACAA 1124
Db      2697 GGGTTATAGTCTCTTCACTTCTATTGACAAAGACAGTTCGACACTTGTCCGACAA 2756
Qy      1125 CTCTTTAGTTAACAATTTAGAGCTAGCTGTTGTGTAACACACTTTTCCAGCAATAG 1184
Db      2757 CTCTTTAGTTAACAATTTAGAGCTAGCTGTTGTGTAACACACTTTTCCAGCAATAG 2816
Qy      1185 TTCTGAGGCAAAAGAGAGCAATGACTTTTAAAGAAAGCTTTCCAGCATCACTTA 1244
Db      2817 TTCTGAGGCAAAAGAGAGCAATGACTTTTAAAGAAAGCTTTCCAGCATCACTTA 2876
Qy      1245 ATCCCAAACTTAAAGAAATGCACTTCCAACTGAGAAAGACTCTGCTGTTGAAAT 1304
Db      2877 ATCCCAAACTTAAAGAAATGCACTTCCAACTGAGAAAGACTCTGCTGTTGAAAT 2936
Qy      1305 AACTTACAGCAGAGAGTCAAGGCGCAGGCAACAGCAACAACAAATTTGGA 1364
Db      2937 AACTTACAGCAGAGAGTCAAGGCGCAGGCAACAGCAACAACAAATTTGGA 2996
Qy      1365 TATATTTCTCACTCACTTTTAAATATACCTTATTTTCTGAGTGAAGAACTAC 1424
Db      2997 TATATTTCTCACTCACTTTTAAATATACCTTATTTTCTGAGTGAAGAACTAC 3056
Qy      1425 AATCAGGCTCTTCACTTATATATATAGTTAAGCTCTTCAAGTACTGTCTT 1484
Db      3057 AATCAGGCTCTTCACTTATATATATAGTTAAGCTCTTCAAGTACTGTCTT 3116
Qy      1485 CTCACCTGAGTATTTTCTTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCC 1544
Db      3117 CTCACCTGAGTATTTTCTTCCCACTTGGCCCTGTTCTCTCTCTCTCTCTCC 3176
Qy      1545 TTGCAAGAGGAATATTTAATATATATGAGTCCAACTCAATATATATATATAT 1604
Db      3177 TTGCAAGAGGAATATTTAATATATATGAGTCCAACTCAATATATATATATAT 3236
Qy      1605 ATTAAGAGATTTAATCTCTTCTAGAAAATGCAAGGCTTAAGCATAGCAACAA 1664
Db      3237 ATTAAGAGATTTAATCTCTTCTAGAAAATGCAAGGCTTAAGCATAGCAACAA 3296
Qy      1665 AGAAGAAATGCAAGAAATTTGCACTGAGAGCAAGCAATCGAATAAATTTTCCAAA 1724
Db      3297 AGAAGAAATGCAAGAAATTTGCACTGAGAGCAAGCAATCGAATAAATTTTCCAAA 3356
Qy      1725 GTTCTTTTATATGATATATGTCAGATTTGAAGAGCTAATTTTAAATGTTGCA 1784
Db      3357 GTTCTTTTATATGATATATGTCAGATTTGAAGAGCTAATTTTAAATGTTGCA 3416
Qy      1785 CTAGCAATCTATCTTCCGAACACAGCAGAGAAATGAAAGTAAAGTAAAGTTATA 1844
Db      3417 CTAGCAATCTATCTTCCGAACACAGCAGAGAAATGAAAGTAAAGTAAAGTTATA 3476
Qy      1845 AATCATTTGTAAGATTTATCCATATATTTTAAATCAAGAAATTTGTATATCTT 1904
Db      3477 AATCATTTGTAAGATTTATCCATATATTTTAAATCAAGAAATTTGTATATCTT 3536
Qy      1905 TAGAATTTGTAATCAATCTTATATGTAATGTAAGTCAATGCTTCTGATTAATAG 1964

```

```

Db      3537 TAGAATTTGTAATCAATCTTATATGTAATGTAAGTCAATGCTTCTGATTAATAG 3596
Qy      1965 ACCAAATATGTAATCTGTAACCAATCAACATATATATATATATATATATAC 2024
Db      3597 ACCAAATATGTAATCTGTAACCAATCAACATATATATATATATATATATAC 3656
Qy      2025 AGCCAAAAAATATATATATATATATATATATATATATATATATATATATATAT 2041
Db      3657 AAAAAAAAAAAAAAAAAA 3673

RESULT 5
ABK69943
ID ABK69943 standard; DNA; 10427 BP.
XX
XX ABK69943;
AC
XX
XX 15-JUL-2002 (first entry)
XX
XX DE Human secreted protein gene 69 genomic DNA fragment #2.
XX
XX Human; ds; secreted protein; gene therapy; immunosuppressive;
XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;
XX vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial;
XX virocidic; fungicidal; ophthalmological; autoimmune disease; neoplasm;
XX rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
XX cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
XX angiodysgenesis; nervous system disorder; Alzheimer's disease; infection;
XX ocular disorder; corneal infection; wound healing; skin aging;
XX epithelial cell proliferation; food additive.
XX
XX Homo sapiens.
XX
XX MO200226931-A2.
XX
XX 04-APR-2002.
XX
XX 24-SEP-2001; 2001MO-US029871.
XX
XX 25-SEP-2000; 2000US-0234925P.
XX
XX 12-JAN-2001; 2001MO-US000911.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsculis G, Duan DR, Rosen CA, Moore PA, Shi Y;
XX Lafleur DW, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;
XX Andrews GA, Mucenski M, Ebner R;
XX
XX WPI; 2002-362489/39.
XX
XX Novel 71 isolated secreted polypeptides and polynucleotides encoding the
XX polypeptides, useful for treating Huntington's disease, sepsis,
XX meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,
XX asthma.
XX
XX Example 2; Page 1452-1455; 1478pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (or its
XX fragment, homologous complement or allelic variant) encoding a human
XX secreted protein (and its fragment, domain, epitope, variant, secreted
XX form and species variant). Also included are a recombinant vector
XX comprising the nucleic acid, a recombinant host cell comprising the
XX vector, an antibody against the secreted protein, a recombinant host cell
XX that expresses the secreted protein and a method of identifying a binding
XX partner of the secreted protein. The nucleic acid and protein are used to
XX prevent, diagnose, treat or ameliorate a medical condition in e.g.
XX humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for
XX example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX infections caused by bacteria, viruses and fungi and ocular disorders
XX e.g. corneal infection. Many other diseases and disorders are listed in
XX

```


QY 1274 AACTGAGAAAAGACTCTGCTTGGATTGAAATGAAAATTACAGACAGAGACTCAGGCGG 1333
 Db 1141 AACTGAGAAAAGACTCTGCTTGGATTGAAATGAAAATTACAGACAGAGACTCAGGCGG 1200
 QY 1334 CAACAACACGACGACAAACAAATTTGGAAATATATCTTCACACTGCGTTTAAATAT 1393
 Db 1201 CAACAACACGACGACAAACAAATTTGGAAATATATCTTCACACTGCGTTTAAATAT 1260
 QY 1394 CATCTT-ATTATTTTTCTAGTAGAGAACTACAAATCAGCCTCTTCAACATTTATATCA 1452
 Db 1261 CATCTTATATTTTTCTAGTAGAGAACTACAAATCAGCCTCTTCAACATTTATATCA 1320
 QY 1453 GTTTATATAGCCTCTTGCAAGTACTTGTCTCTCAGCTAGAGATTTTTTCTCCCGCA 1512
 Db 1321 GTTTATATAGCCTCTTGCAAGTACTTGTCTCTCAGCTAGAGATTTTTTCTCCCGCA 1380
 QY 1513 CTTGCCCCCTGTCT 1572
 Db 1381 CTTGCCCCCTGTCT 1440
 QY 1573 GGGTCCAACTTCAAT 1632
 Db 1441 GGGTCCAACTTCAAT 1500
 QY 1633 AAAATGCAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTA 1692
 Db 1501 AAAATGCAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCTAAGGCT 1560
 QY 1693 AGACAGCAATCTGAT 1752
 Db 1561 AGACAGCAATCTGAT 1620
 QY 1753 TTTGAAAGAGCTATTTTTTTTAAATGTCAGCAAGCTCAGCTTCCGAAAGACAGC 1812
 Db 1621 TTTGAAAGAGCTA-TTTTTTTAAATGTCAGCAAGCTCAGCTTCCGAAAGACAGC 1679
 QY 1813 CAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1872
 Db 1680 CAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1739
 QY 1873 ATTTTAAATTCAGAAAATTTGTTTATCTTTAAATTTGTTTAAATTTGTTTAAAT 1932
 Db 1740 ATTTTAAATTCAGAAAATTTGTTTATCTTTAAATTTGTTTAAATTTGTTTAAAT 1799
 QY 1933 CTATGAGCTCATGCTTCTGATATATATATATATATATATATATATATATATAT 1992
 Db 1800 CTATGAGCTCATGCTTCTGATATATATATATATATATATATATATATATATAT 1859
 QY 1993 CACATTTTATTTAAATATATATATATATATATATATATATATATATATATAT 2041
 Db 1860 CACATTTTATTTAAATATATATATATATATATATATATATATATATATATAT 1908

RESULT 7
 ABK72048
 ID ABK72048 standard; DNA; 1909 BP.
 AC ABK72048;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE DNA encoding human tumour endothelial marker TEM 42.
 XX
 XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 XX Tumour endothelial marker; normal endothelial marker; PEM;
 XX pan-endothelial marker; polycystic kidney disease; psoriasis;
 XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 XX neovascularization; immune response; cytotoxic; antidiabetic; gene;
 XX ophthalmological; antirheumatic; antidiabetic; antipsoriatic; ds.
 XX OS Homo sapiens.
 XX

PN W0200283874-A2.
 XX 24-OCT-2002.
 PD 10-APR-2002; 2002WO-US008253.
 XX 11-APR-2001; 2001US-0282850P.
 XX 06-FEB-2002; 2002US-0354262P.
 XX (UYUO) UNIV JOHNS HOPKINS.
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 PI WPI; 2003-093016/08.
 DR P-PSDB; ABUS4475.
 PT New purified human transmembrane protein, designated as tumor endothelial
 marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 psoriasis.
 PT
 XX
 XX Disclosure; Page 308-309; 374pp; English.
 PS
 XX The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumour angiogenesis, for
 CC identifying an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC sequence represents a human TEM or NEM gene of the invention
 XX
 SO Sequence 1909 BP; 651 A; 345 C; 311 G; 602 T; 0 U; 0 Other;
 Query Match 89.8%; Score 1878.6; DB 7; Length 1909;
 Best local similarity 99.7%; Pred. No. 0; Mismatches 4; Indels 2; Gaps 2;
 Matches 1903; Conservative 0;
 QY 134 GACACCTTTTAAATGACAGAACTAAGTGAAGGATTTGAGTAACTTTGCTTCAATCAAT 193
 Db 1 GACACCTTTTAAATGACAGAACTAAGTGAAGGATTTGAGTAACTTTGCTTCAATCAAT 60
 QY 194 AAAGTCAAAATGATGAGAAACATTTTGTGCTTCACTTCAATACCCGCTGCTCAATTC 253
 Db 61 AAAGTCAAAATGATGAGAAACATTTTGTGCTTCACTTCAATACCCGCTGCTCAATTC 120
 QY 254 TCTACTGATGATTTATGCTTTAAGTAGAATTCAGTGCCAGAGAGAACTTGTGAATTA 313
 Db 121 TCTACTGATGATTTATGCTTTAAGTAGAATTCAGTGCCAGAGAGAACTTGTGAATTA 180
 QY 314 ATTATTTTAAATTTTTTTTTTATCTTTTCAAAAGCATGATTTATTTGTTGATGTTG 373
 Db 181 ATTATTTTAAATTTTTTTTTTATCTTTTCAAAAGCATGATTTATTTGTTGATGTTG 240
 QY 374 CTCTGATACAGACCAATTTCAATAGATGAGAGCTTAAATTTTCCAAAGATATAG 433
 Db 241 CTCTGATACAGACCAATTTCAATAGATGAGAGCTTAAATTTTCCAAAGATATAG 300
 QY 434 ACATGCAAAAGTTTCAATATAAACTGGGCTTAAACAAATTAATTAATTAATTAATAG 493
 Db 301 ACATGCAAAAGTTTCAATATAAACTGGGCTTAAACAAATTAATTAATTAATTAATAG 360
 QY 494 ATTCCCTTCAAGTTTGTGCAAACTGCGCATCAATTAACAAATTTGAGATGTTGAA 553
 Db 361 ATTCCCTTCAAGTTTGTGCAAACTGCGCATCAATTAACAAATTTGAGATGTTGAA 420
 QY 554 AAGCTAGTTATTTTTCAGAGAAATGATTTTCATTTGAACTGTTCTCTTGCAGGCC 613
 Db 421 AAGCTAGTTATTTTTCAGAGAAATGATTTTCATTTGAACTGTTCTCTTGCAGGCC 480

QY 614 ATTTCCCTTTTCTGCGAGTTTAGCAAGTTTAGAGAGATATAGTCATGAAAAAGAG 673
DB 481 ATTTCCCTTTTCTGCGAGTTTAGCAAGTTTAGAGAGATATAGTCATGAAAAAGAG 540
QY 674 GAAGAAAGGGAGAGAGAGAGAGTTAAAAAGTATGCTCAGACCTATGACGTATCC 733
DB 541 GAAGAAAGGGAGAGAGAGAGTTAAAAAGTATGCTCAGACCTATGACGTATCC 600
QY 734 CTTTGCTGTAATATTTTAAGAGAGCTCAGCTTGTGGAACGAGTTTGTATCTTCC 793
DB 601 CTTTGCTGTAATATTTTAAGAGAGCTCAGCTTGTGGAACGAGTTTGTATCTTCC 660
QY 794 ATATTGAGAGAGAGTTTCTGACTGCAATGCACTAGATGTAATTTTATTTTAT 853
DB 661 ATATTGAGAGAGTTTCTGACTGCAATGCACTAGATGTAATTTTATTTTAT 720
QY 854 CATCTGAGAAAGCTTGTGCTGTAATTAATTAATTTGAGGTTTCTGTCTCATATCT 913
DB 721 CATCTGAGAAAGCTTGTGCTGTAATTAATTAATTTGAGGTTTCTGTCTCATATCT 780
QY 914 GGCCTGATGTCAGAGAGAGAGAGATGAAATGTAATCTCCACATCCAGCATCGA 973
DB 781 GGCCTGATGTCAGAGAGAGAGATGAAATGTAATCTCCACATCCAGCATCGA 840
QY 974 AACCCAAAGGGGTAGGCAATTTCTATGTAAGTTTGGACATGAAAGTTTGTGCTTGT 1033
DB 841 AACCCAAAGGGGTAGGCAATTTCTATGTAAGTTTGGACATGAAAGTTTGTGCTTGT 900
QY 1034 TATGCTGCTCACTGCTATTAACCTCTGCTGCTTATGCTTCTTATCTATTTAGCA 1093
DB 901 TATGCTGCTCACTGCTATTAACCTCTGCTGCTTATGCTTCTTATCTATTTAGCA 960
QY 1094 AGCAGTATCGAACACTTCTGCTGCAAGGCTCTTATGTAATTAATTTAGCAGTATG 1153
DB 961 AGCAGTATCGAACACTTCTGCTGCAAGGCTCTTATGTAATTAATTTAGCAGTATG 1020
QY 1154 TTTGTGTTAAACAACCTTTTCAACCAATAGTTTCTGAGGCAAGAGCAATGACTAT 1213
DB 1021 TTTGTGTTAAACAACCTTTTCAACCAATAGTTTCTGAGGCAAGAGCAATGACTAT 1080
QY 1214 TAAAGAAAGGCTTCCGACATCACTTACATCCCAAACTAATAAGATCACTTCC 1273
DB 1081 TAAAGAAAGGCTTCCGACATCACTTACATCCCAAACTAATAAGATCACTTCC 1140
QY 1274 AACTGAGAAAGACTCTGCTGCTGTAATGAAACTTACAGAGAGTCAAGGCCACGG 1333
DB 1141 AACTGAGAAAGACTCTGCTGCTGTAATGAAACTTACAGAGAGTCAAGGCCACGG 1200
QY 1334 CAAGCAACAGCAACAACAACATTTGGAATATTAATCTCACTCAGCTTTATATATA 1393
DB 1201 CAAGCAACAGCAACAACAACATTTGGAATATTAATCTCACTCAGCTTTATATATA 1260
QY 1394 CATCTT-ATTAATTTTCTAGTAGAGAACTAACAATGACCTCTTCAACATTTATATCA 1452
DB 1261 CATCTTATTAATTTTCTAGTAGAGAACTAACAATGACCTCTTCAACATTTATATCA 1320
QY 1453 GTTATAATAGCTCTTGAAGTACTTGTCTCTCACTGAGAGATTTTCTCTCCCA 1512
DB 1321 GTTATAATAGCTCTTGAAGTACTTGTCTCTCACTGAGAGATTTTCTCTCCCA 1380
QY 1513 CTTGCGCCCTGTCT 1572
DB 1381 CTTGCGCCCTGTCT 1440
QY 1573 GGGTCCAACTTCAAT 1632
DB 1441 GGGTCCAACTTCAAT 1500
QY 1633 AAAATGCAAGGCTAGAGCATAGACAAACAAGAAATGCTGAGAAATTTGCCACTGG 1692
DB 1501 AAAATGCAAGGCTAGAGCATAGACAAACAAGAAATGCTGAGAAATTTGCCACTGG 1560

QY 1693 AGACAGCAATCTGATATATATATTTGCCAAAAGTTCTTTTATGTCATATAGTCAGGA 1752
DB 1561 AGACAGCAATCTGATATATATATTTGCCAAAAGTTCTTTTATGTCATATAGTCAGGA 1620
QY 1753 TTTGAGAGAGCTATTTTATATGTTGCAACTAGCAACTCATCTTGGAGAGACAGC 1812
DB 1621 TTTGAGAGAGCTA-TTTTATATGTTGCAACTAGCAACTCATCTTGGAGAGACAGC 1679
QY 1813 CAGAGAAATGAGTAGAGAGAGAGTTTATTAATTCATTTGTAAGCATTTATCCATAT 1872
DB 1680 CAGAGAAATGAGTAGAGAGAGTTTATTAATTCATTTGTAAGCATTTATCCATAT 1739
QY 1873 ATTTTAATTTCAAGAAAATTTGCTTTATCTTTGAAATTTGTAATCTTATGTA 1932
DB 1740 ATTTTAATTTCAAGAAAATTTGCTTTATCTTTGAAATTTGTAATCTTATGTA 1799
QY 1933 CTATGTACTCATGCTTCTGATTAATAAAGACCAATATGATCTGTAACCAATCA 1992
DB 1800 CTATGTACTCATGCTTCTGATTAATAAAGACCAATATGATCTGTAACCAATCA 1859
QY 1993 CACATTTATATTAATATATATCTATATTAACAGCCAAAAAATTTTATTTT 2041
DB 1860 CACATTTATATTAATATATATCTATATTAACAAAAAATTTTATTTTATTTT 1908

RESULT 8
ABV25337
ID ABV25337 standard; cDNA; 3461 BP.
XX
XX ABV25337;
XX
DT 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker CDNA 25328.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
XX 25-MAY-2000; 2000US-0207454P.
XX
XX 09-JUN-2000; 2000US-0211314P.
XX
XX 18-JUL-2000; 2000US-0219007P.
XX
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 4991-4992; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (i) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX

(f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

Query Match 65.4%; Score 1366.6; DB 5; Length 3461;
Best Local Similarity 94.5%; Pred. No. 8.4e-275;
Matches 1498; Conservative 0; Mismatches 15; Indels 73; Gaps 5;

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 3461 BP; 1128 A; 638 C; 590 G; 1104 T; 0 U; 1 Other;

Query Match 65.4%; Score 1366.6; DB 5; Length 3461;
Best Local Similarity 94.5%; Pred. No. 8.4e-275;
Matches 1498; Conservative 0; Mismatches 15; Indels 73; Gaps 5;

QY 1 AAGAGACAGACTATTAACTCCACAGTAAATTAAGACGTATGTCATGTTTATTGTTA 60
DB AAGAGACAGACTATTAACTCCACAGTAAATTAAGACGTATGTCATGTTTATTGTTA 1990
QY 61 AAGCAGTGTGATGATGCTTCAAGCATGTAATCTTCATCTCCCGC----- 111
DB AAGCAGTGTGATGATGCTTCAAGCATGTAATCTTCATCTCCCGC----- 2050
QY 112 -----CGTTTGTGTTCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 164
DB ACACACACACTTTTGTGTTCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 2051
QY 165 CATTTCATTAAGTCTTTCATTAATCAATTAAGTCAATGTAAGAACTTTGTGCC 224
DB CATTTCATTAAGTCTTTCATTAATCAATTAAGTCAATGTAAGAACTTTGTGCC 2110
QY 2111 CATTTCATTAAGTCTTTCATTAATCAATTAAGTCAATGTAAGAACTTTGTGCC 2170
DB CATTTCATTAAGTCTTTCATTAATCAATTAAGTCAATGTAAGAACTTTGTGCC 2170
QY 225 TACTCTCATACCCCGTACTCAAAATCTCTACTGATGATTAATGCTTTAGTAGAAT 284
DB TACTCTCATACCCCGTACTCAAAATCTCTACTGATGATTAATGCTTTAGTAGAAT 2171
QY 2171 TACTCTCATACCCCGTACTCAAAATCTCTACTGATGATTAATGCTTTAGTAGAAT 2230
DB TACTCTCATACCCCGTACTCAAAATCTCTACTGATGATTAATGCTTTAGTAGAAT 2230
QY 285 TAGAGCCCAAGAGAACTTGGTGAATTAATTTTATTTTATTTTATCCCTTACA 344
DB TAGAGCCCAAGAGAACTTGGTGAATTAATTTTATTTTATTTTATCCCTTACA 2231
QY 2231 TAGAGCCCAAGAGAACTTGGTGAATTAATTTTATTTTATTTTATCCCTTACA 2290
DB TAGAGCCCAAGAGAACTTGGTGAATTAATTTTATTTTATTTTATCCCTTACA 345
QY AAGCAGTGTGATGCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 404
DB AAGCAGTGTGATGCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 2291
QY 2291 AAGCAGTGTGATGCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 405
DB AAGCAGTGTGATGCTTTCAGTAGACACCTTTTAAATGCAACTAACTAGAG 2350
QY 405 GCTGTTAATTTTCCAAAGAGTAAATGACATGCAAAAGTTTCAATTAATCTGGCCA 464
DB GCTGTTAATTTTCCAAAGAGTAAATGACATGCAAAAGTTTCAATTAATCTGGCCA 2351
QY 2351 GCTGTTAATTTTCCAAAGAGTAAATGACATGCAAAAGTTTCAATTAATCTGGCCA 2410
DB GCTGTTAATTTTCCAAAGAGTAAATGACATGCAAAAGTTTCAATTAATCTGGCCA 465
QY 465 TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
DB TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2411
QY 2411 TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 525
DB TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2471
QY 525 TCCAAATAACAAATTTGAGATGCTGTAAGAAAGCTAATTAATTCAGAGAAATGATTC 584
DB TCCAAATAACAAATTTGAGATGCTGTAAGAAAGCTAATTAATTCAGAGAAATGATTC 2471
QY 584 ATTATTTGAAACGTCTCCCTAGAGGCAATTTCCCTTTCCGGAGTTTAGCAAGT 644
DB ATTATTTGAAACGTCTCCCTAGAGGCAATTTCCCTTTCCGGAGTTTAGCAAGT 2531
QY 2531 ATTATTTGAAACGTCTCCCTAGAGGCAATTTCCCTTTCCGGAGTTTAGCAAGT 645
DB ATTATTTGAAACGTCTCCCTAGAGGCAATTTCCCTTTCCGGAGTTTAGCAAGT 2591
QY 645 TTAGAGAGAAATGATCATGAAAGAAAGAGAAAGAGAGAGAGAGAGAGTTAAAA 704
DB TTAGAGAGAAATGATCATGAAAGAAAGAGAAAGAGAGAGAGAGAGAGTTAAAA 2591
QY 2591 TTAGAGAGAAATGATCATGAAAGAAAGAGAAAGAGAGAGAGAGAGAGTTAAAA 705
DB TTAGAGAGAAATGATCATGAAAGAAAGAGAAAGAGAGAGAGAGAGAGTTAAAA 2651
QY 705 GTAAGTGTCTCAGACCTATGAAAGTAACTCCCTTTGCTAAGAAATTTAAGACAGTCA 764
DB GTAAGTGTCTCAGACCTATGAAAGTAACTCCCTTTGCTAAGAAATTTAAGACAGTCA 2651
QY 2651 GTAAGTGTCTCAGACCTATGAAAGTAACTCCCTTTGCTAAGAAATTTAAGACAGTCA 765
DB GTAAGTGTCTCAGACCTATGAAAGTAACTCCCTTTGCTAAGAAATTTAAGACAGTCA 2710
QY 765 TTGATTGAAACTGAGTTTGTTCATCTTCATTTTGAGAGAAAGTATTTTCTGACTGCA 824
DB TTGATTGAAACTGAGTTTGTTCATCTTCATTTTGAGAGAAAGTATTTTCTGACTGCA 2711
QY 2711 TTGATTGAAACTGAGTTTGTTCATCTTCATTTTGAGAGAAAGTATTTTCTGACTGCA 825
DB TTGATTGAAACTGAGTTTGTTCATCTTCATTTTGAGAGAAAGTATTTTCTGACTGCA 2771
QY 825 ATGCACTGATGATTAATTTTATTTTATCATCTTGAAGAAAGCTTGAATTAAGAAATGA 884
DB ATGCACTGATGATTAATTTTATTTTATCATCTTGAAGAAAGCTTGAATTAAGAAATGA 2771
QY 2771 ATGCACTGATGATTAATTTTATTTTATCATCTTGAAGAAAGCTTGAATTAAGAAATGA 885
DB ATGCACTGATGATTAATTTTATTTTATCATCTTGAAGAAAGCTTGAATTAAGAAATGA 2830
QY 885 TAAATTTGAGGTTTCTGCTCATCTGCTTGCATGTCAGAGAAAGCAGAGATAGA 944
DB TAAATTTGAGGTTTCTGCTCATCTGCTTGCATGTCAGAGAAAGCAGAGATAGA 2830

DB 2831 TAAATTTGAGGTTTCTGCTCATCTGCTTGCATGTCAGAGAAAGCAGAGATAGA 2890
QY 945 AATGTAATCTCCATCATCCAGCATTCGAAACCAAGGGGTAGGAATTCATATGAGTT 1004
DB AATGTAATCTCCATCATCCAGCATTCGAAACCAAGGGGTAGGAATTCATATGAGTT 2891
QY 1005 TTGACATGAAGTTTGTGATCTTGTGATGCTGCTCAACTGATTAATTAACCTCTCT 1064
DB TTGACATGAAGTTTGTGATCTTGTGATGCTGCTCAACTGATTAATTAACCTCTCT 2951
QY 2951 TTGACATGAAGTTTGTGATCTTGTGATGCTGCTCAACTGATTAATTAACCTCTCT 1065
DB TTGACATGAAGTTTGTGATCTTGTGATGCTGCTCAACTGATTAATTAACCTCTCT 3011
QY 3011 GGTATTAATCTCTTCAATTTTGAAGCAAGCATGAACTTGTGCAAGAG 3070
DB GGTATTAATCTCTTCAATTTTGAAGCAAGCATGAACTTGTGCAAGAG 1125
QY 1125 CTCTTATGTTAACTTTAGCAGTACTGTTTGTGTTAAACAATTTTCAACCAATAGG 1184
DB CTCTTATGTTAACTTTAGCAGTACTGTTTGTGTTAAACAATTTTCAACCAATAGG 3071
QY 3071 CTCTTATGTTAACTTTAGCAGTACTGTTTGTGTTAAACAATTTTCAACCAATAGG 1185
DB CTCTTATGTTAACTTTAGCAGTACTGTTTGTGTTAAACAATTTTCAACCAATAGG 3131
QY 3131 TTCTGAGGCAACGAGAGCATGATGATTTTAAAGAAAGCTTTCCAGATCATTAAC 1244
DB TTCTGAGGCAACGAGAGCATGATGATTTTAAAGAAAGCTTTCCAGATCATTAAC 3191
QY 3191 ATCCCAAACTAAAAAGATCACTCTTCCACTGAGAAAGACTCTGCTTTGATGGA 1304
DB ATCCCAAACTAAAAAGATCACTCTTCCACTGAGAAAGACTCTGCTTTGATGGA 1305
QY 1305 AACTTACAGAGAGAGTCAAGGCCAGGCAACAAACAGACAAACAAATTTGAA 1364
DB AACTTACAGAGAGAGTCAAGGCCAGGCAACAAACAGACAAACAAATTTGAA 3227
QY 3227 -----AACCAACAGAGAAACAAACAAATTTGAA 1365
DB -----AACCAACAGAGAAACAAACAAATTTGAA 3257
QY 3257 TATTAATTCATCTCAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1424
DB TATTAATTCATCTCAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3317
QY 3317 AAATCAGCTCTTCAACACTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1484
DB AAATCAGCTCTTCAACACTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 3377
QY 3377 TCTCAGCTGAGGATTTTCTTCTCCGCACTTGGCCCGCTGCTCCCTCTCTCTCC 1543
DB TCTCAGCTGAGGATTTTCTTCTCCGCACTTGGCCCGCTGCTCCCTCTCTCTCC 1544
QY 1544 CTTTGCAGAGAGAAATTAATTAACATA 1569
DB CTTTGCAGAGAGAAATTAATTAACATA 3435
QY 3435 CTTTGCAGAGAGAAATTAATTAACATA 3460
DB CTTTGCAGAGAGAAATTAATTAACATA 3460

RESULT 9
ABT10123/c
ID ABT10123 standard; cDNA; 594 BP.
XX
XX ABT10123;
AC
XX
XX
DT 04-DEC-2002 (first entry)
XX
XX Human breast cancer associated coding sequence SEQ ID NO: 257.
XX Human; breast specific gene; breast cancer; differential expression;
XX cytostatic; gene therapy; gene; ss.
XX Homo sapiens.
XX
XX WO200259271-A2.
XX
XX
XX 01-AUG-2002.
XX
XX
XX 25-JAN-2002; 2002WO-US002176.
XX
XX 25-JAN-2001; 2001US-02637572.
XX 25-APR-2001; 2001US-0286090P.
XX 23-MAY-2001; 2001US-0292517P.
XX
XX (GENE-) GENE LOGIC INC.
PA

XX Orr MS, Nation M, Diggins JC, Zeng W;
XX WPI; 2002-674803/72.
XX
XX
XX Diagnosing breast cancer in a patient comprises detecting the level of
XX gene expression in cell or tissue samples, where a differential gene
XX expression is indicative of breast cancer.
XX
XX Claim 1; SEQ ID NO 257; 260bp + Sequence Listing; English.
XX
XX The present invention relates to methods of diagnosing breast cancer in a
XX patient, which comprise detecting the level of expression in a tissue
XX sample of two or more genes selected from those shown in ABR09867-
XX ABR1112, where a differential expression of the genes indicates breast
XX cancer. The methods are useful in diagnosing, treating, detecting the
XX progression, and in monitoring treatment of breast cancer in patients.
XX The methods are also useful as a screening tool for agents that modulate
XX the onset or progression of breast cancer. The breast cancer genes may be
XX used as diagnostic markers for the prediction or identification of the
XX malignant state of breast tissue, for confirming the type and progression
XX of cancer, and for drug screening and assays. The present sequence is a
XX coding sequence of the invention. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 594 BP; 204 A; 81 C; 110 G; 198 T; 0 U; 1 Other;
XX
XX Query Match 28.3%; Score 591.4; DB 6; Length 594;
XX Best Local Similarity 99.7%; Pred. No. 1.5e-113;
XX Matches 592; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1431 GCGCTTTCAACATTATATACAGTTAAAGAGCTTGGCAAGTACTGTTCTCTAC 1490
DB 594 GCGCTTTCAACATTATATACAGTTAAAGAGCTTGGCAAGTACTGTTCTCTAC 535
QY 1491 TGAGGATTTTCTCCGCCACCTGGCCCGTTCCTCCCTCTCCCTCCCTTGGCA 1550
DB 534 TGAGGATTTTCTCCGCCACCTGGCCCGTTCCTCCCTCTCCCTCTCCCTTGGCA 475
QY 1551 AGAGGAATATTTAAATATTTGGTCCCACTCAATATATATATATATATATTA 1610
DB 474 AGAGGAATATTTAAATATTTGGTCCCACTCAATATATATATATATATATTA 415
QY 1611 AGCATTTAATCTCTCTTCTAGAAAATGCAAGGCTAGGATGACAAACAAAGGAA 1670
DB 414 AGCATTTAATCTCTCTTCTAGAAAATGCAAGGCTAGGATGACAAACAAAGGAA 355
QY 1671 ATGCTGAGAAATTTGCCACTGAGAGCAAGCAATGTAATTAATTTGCCAAAGTCTT 1730
DB 354 ATGCTGAGAAATTTGCCACTGAGAGCAAGCAATGTAATTAATTTGCCAAAGTCTT 295
QY 1731 TTTATGTCATATAGTGTCAGATTTTGAAGAGCTTTTCTTTTATGTTGCACTAGCA 1790
DB 294 TTTATGTCATATAGTGTCAGATTTTGAAGAGCTTTTCTTTTATGTTGCACTAGCA 235
QY 1791 ACTCATCTTGGAGAGACAGCCAGAGAAATGAATAGTAGAAGTTATATATCA 1850
DB 234 ACTCATCTTGGAGAGACAGCCAGAGAAATGAATAGTAGAAGTTATATATCA 175
QY 1851 TTTGTAAGCAATTTCCATATATTTTAAATCAAGAAAAATGTGTTATCTTTAGAT 1910
DB 174 TTTGTAAGCAATTTCCATATATTTTAAATCAAGAAAAATGTGTTATCTTTAGAT 115
QY 1911 TTTGTAATCAATTTATATATATATATATATATATATATATATATATATATAT 1970
DB 114 TTTGTAATCAATTTATATATATATATATATATATATATATATATATATATAT 55
QY 1971 TATGATCTGTAAACCAATCAATCATATATATATATATATATATATATATAC 2024
DB 54 TATGATCTGTAAACCAATCAATCATATATATATATATATATATATATATATAC 1

RESULT 10
ABX74748
ID ABX74748 standard; cDNA; 488 BP.
XX
XX AC ABX74748;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human cDNA sequence #1 up-regulated in CC-RCC patients.
XX
XX KW Human; microarray; solid surface; immobilised probe; CC-RCC;
XX differential expression profile; aggressive CC-RCC tumour type;
XX non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
XX KW gene expression profiling; tumour tissue; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200279411-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002WO-US009576.
XX
XX PR 29-MAR-2001; 2001US-0279411P.
XX
XX PA (VAND-) VAN ANDEL INST.
XX
XX PI Haab B, Rhodes D, Teh BT, Takashi M,
XX
XX DR WPI; 2003-040679/03.
XX
XX PT New microarray, comprising a matrix of cDNA probe from a set of probes
XX immobilised to a solid surface in predetermined order, useful in the
XX prognosis of patients with clear cell renal carcinoma.
XX
XX PS Claim 35; SEQ ID NO 141; 179bp; English.
XX
XX The present invention relates to a microarray comprising a matrix of at
XX least one cDNA probe from a set of probes immobilised to a solid surface
XX in a predetermined order, where a row of pixels corresponds to replicates
XX of one predetermined probe from the set. The probes are complementary to
XX nucleic acid sequences that are expressed differentially in aggressive as
XX compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)
XX and that hybridise to the probes under high stringency conditions. The
XX microarray is useful for the prognosis of patients with CC-RCC, wherein
XX aggressive and non-aggressive CC-RCC tumour types are characterised by
XX differential expression profiles of genes that hybridise with one or more
XX probes immobilised on the microarray. The arrays are useful for gene
XX expression profiling of tumour and normal tissues. The present sequence
XX represents a human cDNA sequence up-regulated in CC-RCC patients
XX
XX Sequence 488 BP; 151 A; 122 C; 69 G; 145 T; 0 U; 1 Other;
XX
XX Query Match 20.4%; Score 425.8; DB 7; Length 488;
XX Best Local Similarity 98.6%; Pred. No. 4.5e-79;
XX Matches 482; Conservative 0; Mismatches 2; Indels 5; Gaps 5;
XX
QY 1070 ATAGTCTCTTCAATTTAGACAGACAGTATGAAAGCTTGGCTTGGCAAGGCTCTT 1129
DB 2 ATAGTCTCTTCAATTTAGACAGACAGTATGAAAGCTTGGCTTGGCAAGGCTCTT 60
QY 1130 TAGTTAAACAATTTAGAGAGCTAGTGTGTGTTAAACACACTTTTCCACAAATAGTTCTG 1189
DB 61 TAGTTAAACAATTTAGAGAGCTAGTGTGTGTTAAACACACTTTTCCACAAATAGTTCTG 120
QY 1190 AGGCAACGAGAGCAATGACTATTTTAAAGAAAGCTTCCAGCATCACTTACATCC 1249
DB 121 AGGCAACGAGAGCAATGACTATTTTAAAGAAAGCTTCCAGCATCACTTACATCC 180
QY 1250 AAAAATGTAAGTCACTCTTCCAACTGAGAAAGAAAGCTCTGCTTTGATGAAACTT 1309
DB 181 AAAAATGTAAGTCACTCTTCCAACTGAGAAAGAAAGCTCTGCTTTGATGAAACTT 240

Db 31 ATTATATTAAATATATATCTATATACAGCC 1
 RESULT 12
 ABL66826/c
 ID ABL66826 standard; DNA; 331 BP.
 AC ABL66826;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:5163.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytoskeletal; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US010838.
 XX
 PR 05-JUN-2000; 2000US-02095473P.
 PR 05-JUN-2000; 2000US-02095313P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Sopet DR, Weaver Z;
 XX
 DR WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 PS Claim 1; SEQ ID NO 5163; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX
 SO Sequence 331 BP; 118 A; 47 C; 48 G; 118 T; 0 U; 0 Other;
 XX
 Query Match 15.8%; Score 331; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 2.3e-59;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1698 AGCAATCTGATTAATATATTTGCCAAAGTCTTTTATGTCATATAGTTCAGATTGA 1757
 Db 331 AGCAATCTGATTAATATTTGCCAAAGTCTTTTATGTCATATAGTTCAGATTGA 272
 QY 1758 AGAGCTATTTTATTTTATGTCACATGACATCTTCGGAAGACAGCCAGGA 1817
 Db 271 AGAGCTATTTTATTTTATGTCACATGACATCTTCGGAAGACAGCCAGGA 212
 QY 1818 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCATTTATCCATATATTT 1877
 Db 211 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCATTTATCCATATATTT 152
 QY 1878 AAATTCAGAAAATGTTTATGTTTGAATTTGATTCATATCTTTAGTACTATG 1937
 Db 151 AAATTCAGAAAATGTTTATGTTTGAATTTGATTCATATCTTTAGTACTATG 92
 QY 1938 TGACTCATGCTTCTGATTAATTAAGACACCAATATGATGTAACCAATCACAT 1997
 Db 91 TGACTCATGCTTCTGATTAATTAAGACACCAATATGATGTAACCAATCACAT 32
 QY 1998 ATTATATTAAATATATCTATATTAACAGCC 2028
 Db 31 ATTATATTAAATATATCTATATTAACAGCC 1
 RESULT 13
 ABL94862/c
 ID ABL94862 standard; DNA; 331 BP.
 AC ABL94862;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #1360 used to diagnose liver cancer.
 DE
 DE Gene; liver cancer; ds; hepatocellular carcinoma; hepatocellular;
 KW metastatic liver tumour; cytoskeletal; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

11173.750 Million cell updates/sec

Title: US-09-646-569A-60

Sequence: 1 aagagacagactattactc.....ggagagaaggggggaggt 2091

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

GenEmbl.*

- 1: gb.ba.*
- 2: gb.hg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.secs.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.secs.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.hg.hum.*
- 31: em.hg.in.*
- 32: em.hg.other.*
- 33: em.hg.mus.*
- 34: em.hg.pln.*
- 35: em.hg.rod.*
- 36: em.hg.mam.*
- 37: em.hg.vrt.*
- 38: em.sv.*
- 39: em.hgo.hum.*
- 40: em.hgo.mus.*
- 41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2091	100.0	2091	6	AX017512 Sequence
2	2091	100.0	2091	5	BD135202 Human nuc
3	2036	97.4	2411	6	AX017611 Sequence
4	2036	97.4	2411	6	BD135230 Human nuc
5	2003.8	95.8	3674	6	BD218591 71 human
6	2001.2	95.7	5683	6	BK537427 Homo sapi
7	2000.6	95.7	191699	2	AC031977 Homo sapi
8	1997.4	95.5	165329	9	AL583850 Human DNA
9	1878.6	89.8	1909	6	AX393338 Sequence
10	1853.4	88.6	6005	6	AK379936 Sequence
11	1845.6	88.3	1463	9	AK026775 Homo sapi
12	1225.6	58.6	1490	9	BC029357 Homo sapi
13	1112	53.2	1121	9	AL157502 Homo sapi
14	331	15.8	331	6	AX330124 Sequence
15	331	15.8	331	6	AX334654 Sequence
16	331	15.8	331	6	AX408713 Sequence
17	210	10.0	224486	2	AC115766 Sequence
18	160.4	7.7	1316	10	AC115766 Mus muscu
19	155	7.4	275631	6	BC005656 Rattus no
20	136	6.5	140	6	AX901039 Sequence
21	136	6.5	140	6	BD036572 Sequence
22	95.2	4.6	547	6	AX401089 Sequence
23	74.8	3.6	229692	2	BK649311 Danto rer
24	70	3.3	110000	2	PFMA13_00 Plasmodiu
25	69	3.3	176785	2	AC118849 Mus muscu
26	68.8	3.3	275530	2	BK572620 Danto rer
27	67.6	3.2	181238	2	BK664607 Danto rer
28	67.2	3.2	103344	9	HS1100E15 Human DNA
29	67.2	3.2	182477	2	BK649274 Danto rer
30	67.2	3.2	252420	2	AE014841 Plasmodiu
31	66.8	3.2	212487	2	BK649365 Mus muscu
32	66.6	3.2	2108	3	PF627 Plasmodiu
33	66.2	3.2	170131	6	BK666066 Danto rer
34	65.8	3.1	347582	3	PFMA14P1 Plasmodiu
35	65.4	3.1	301	6	BD244186 Compounds
36	65.4	3.1	301	6	AR237369 Sequence
37	65.4	3.1	301	6	AR260862 Sequence
38	65.4	3.1	301	6	AR278933 Sequence
39	65.4	3.1	301	6	AR367089 Sequence
40	65.4	3.1	301	6	AR370985 Sequence
41	65.4	3.1	301	6	AR392490 Sequence
42	65.4	3.1	301	6	AR400125 Sequence
43	65.4	3.1	301	6	AR405392 Sequence
44	65.4	3.1	301	6	AX106499 Sequence
45	65.4	3.1	301	6	AX140790 Sequence

ALIGNMENTS

RESULT 1				
AX017512				
LOCUS	AX017512	2091 bp	DNA	linear
DEFINITION	Sequence 60 from Patent WO9947655.			PAT 07-SEP-2000
ACCESSION	AX017512			
VERSION	AX017512.1			
KEYWORDS	GI:10042309			
SOURCE	.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Schmitz,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Platarsky,C.			
TITLE	Human nucleic acid sequences from normal breast tissue			

JOURNAL

Parent: WO 9947655-A 60 23-SEP-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
 BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
 (DE); PILARSKY CHRISTIAN (DE)
 Location/Qualifiers

FEATURES

1..2091
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2091; DB 6; Length 2091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AAGAGACAGCATTAATCCACAGTAAATAGAGCATATGTTCCATGTTATTTGTA 60
Db 1 AAGAGACAGCATTAATCCACAGTAAATAGAGCATATGTTCCATGTTATTTGTA 60
QY 61 AAGCAGTGTGATAGCCTTCAAGCATGTGAATATCTTCATCTTCCCGCGCTTTTG 120
Db 61 AAGCAGTGTGATAGCCTTCAAGCATGTGAATATCTTCATCTTCCCGCGCTTTTG 120
QY 121 TTTCTTTCAAGTACACCTTTTAAATGCGAATACTAGAGCATTTCACTAGT 180
Db 121 TTTCTTTCAAGTACACCTTTTAAATGCGAATACTAGAGCATTTCACTAGT 180
QY 181 CTTTCAATCAATTAAGTCAAAATGTATGGAACATTTTGCCCTACTCTCCATACCCCG 240
Db 181 CTTTCAATCAATTAAGTCAAAATGTATGGAACATTTTGCCCTACTCTCCATACCCCG 240
QY 241 TGTACTCAATCTCTACTGTATGTAATATGCTTTAAGTAATTCATGTCAGAGAGAA 300
Db 241 TGTACTCAATCTCTACTGTATGTAATATGCTTTAAGTAATTCATGTCAGAGAGAA 300
QY 301 CTGCGGAATTAATATTTATTTTATCTTTATCTTTACCAAGCCATGGATTTTAT 360
Db 301 CTGCGGAATTAATATTTATTTTATCTTTATCTTTACCAAGCCATGGATTTTAT 360
QY 361 TGGTGTATGTGCTGTGTACCAAGCCATTTCAATAGATGAGCTGTATTTTTC 420
Db 361 TGGTGTATGTGCTGTGTACCAAGCCATTTCAATAGATGAGCTGTATTTTTC 420
QY 421 CAAGAGTAATGACATGCAAAAGTTCAATAAAACTGGCCATTAACTAAATTA 480
Db 421 CAAGAGTAATGACATGCAAAAGTTCAATAAAACTGGCCATTAACTAAATTA 480
QY 481 TAAACTATATAGCATTCCTTTAGGTTTTTTCGCAACTGCTATTCGAATTAATTTG 540
Db 481 TAAACTATATAGCATTCCTTTAGGTTTTTTCGCAACTGCTATTCGAATTAATTTG 540
QY 541 AGAATGTTGAATAAAGCTAGTTATTTTCAAGAAATGATTTTCATTATTTGAACGTTTC 600
Db 541 AGAATGTTGAATAAAGCTAGTTATTTTCAAGAAATGATTTTCATTATTTGAACGTTTC 600
QY 601 TCCCTAGCAGGCAATTTCCCTTTTCTGAGAGTTTACCAAGTTTGAAGAGAAATAGTC 660
Db 601 TCCCTAGCAGGCAATTTCCCTTTTCTGAGAGTTTACCAAGTTTGAAGAGAAATAGTC 660
QY 661 ATGAAAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 ATGAAAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ATGAAGCTAATCCCTTTGCTAGAAATATTTAAGAGAGCTCAGCTTGTTGAAGTGAAT 780
Db 721 ATGAAGCTAATCCCTTTGCTAGAAATATTTAAGAGAGCTCAGCTTGTTGAAGTGAAT 780
QY 781 TTTGTCACTTCCATATTTGCAAGAGAGATTTTTCAGACTTGAATGCAAGCTAGATGTA 840
Db 781 TTTGTCACTTCCATATTTGCAAGAGAGATTTTTCAGACTTGAATGCAAGCTAGATGTA 840
QY 841 AATTTATTTATCATCTAGAAAGCTTACTAGAAAAATGAATTAATTTAGAGGTTT 900
Db 841 AATTTATTTATCATCTAGAAAGCTTACTAGAAAAATGAATTAATTTAGAGGTTT 900

```

```

Db 841 AATTTATTTATCATCTAGAAAGCTTACTAGAAAAATGAATTAATTTAGAGGTTT 900
QY 901 CCGTCCATATATGCTGTGATGTCCAGAAAAAGCAGAAATAGAAATGTATCTCCAAC 960
Db 901 CCGTCCATATATGCTGTGATGTCCAGAAAAAGCAGAAATAGAAATGTATCTCCAAC 960
QY 961 ATCCAAAGCATGAAACCCAGGGGTAGGCAATTCATAGTGTTTTGGACATGAGTTTG 1020
Db 961 ATCCAAAGCATGAAACCCAGGGGTAGGCAATTCATAGTGTTTTGGACATGAGTTTG 1020
QY 1021 GTGCATCTTGTTTATGCTGCTCAACTGCTATTAACCTCTGCTTAATAGTCTTTC 1080
Db 1021 GTGCATCTTGTTTATGCTGCTCAACTGCTATTAACCTCTGCTTAATAGTCTTTC 1080
QY 1081 ATTCTATTAAGACAAGCATATCGAACACTTTCCTTGGCAAGAGCTTTAATTAACAT 1140
Db 1081 ATTCTATTAAGACAAGCATATCGAACACTTTCCTTGGCAAGAGCTTTAATTAACAT 1140
QY 1141 TTAGCAGCTACTGTTTGTGTAAACACACTTTCACAAATAGTTCAGAGCAACGAG 1200
Db 1141 TTAGCAGCTACTGTTTGTGTAAACACACTTTCACAAATAGTTCAGAGCAACGAG 1200
QY 1201 AGCAATGACTATTTAAAGAAAGCTTCCAGCATCATTAACATCCCAAACTTAATA 1260
Db 1201 AGCAATGACTATTTAAAGAAAGCTTCCAGCATCATTAACATCCCAAACTTAATA 1260
QY 1261 GATCACTCTTCCACTGAGAAAGACCTGCGCTTGAATGGAACCTTACAGAGAGAG 1320
Db 1261 GATCACTCTTCCACTGAGAAAGACCTGCGCTTGAATGGAACCTTACAGAGAGAG 1320
QY 1321 TCACAGGCGCAGGCAACAACAGCAACAACAACATTTGAAATATTTCTCACTCA 1380
Db 1321 TCACAGGCGCAGGCAACAACAGCAACAACAACATTTGAAATATTTCTCACTCA 1380
QY 1381 CGTTTAAATATACATCTTATTTATTTTCTAGAGAGAACTACAAATCAGCTCTTCA 1440
Db 1381 CGTTTAAATATACATCTTATTTATTTTCTAGAGAGAACTACAAATCAGCTCTTCA 1440
QY 1441 CATTATATACAGTTTAAATAGCCTGTGCAAGTTACTGTCTGACCTGAGTATTT 1500
Db 1441 CATTATATACAGTTTAAATAGCCTGTGCAAGTTACTGTCTGACCTGAGTATTT 1500
QY 1501 TTTTCTCCCGACCTTGGCCCTCTTCTGCTCCCTCTGCTTCCCTTGGCAAGAGAAAT 1560
Db 1501 TTTTCTCCCGACCTTGGCCCTCTTCTGCTCCCTCTGCTTCCCTTGGCAAGAGAAAT 1560
QY 1561 TTTAACATATTTGGGTCACATCTCAATATATATATATATATATATATATATATAT 1620
Db 1561 TTTAACATATTTGGGTCACATCTCAATATATATATATATATATATATATATATATAT 1620
QY 1621 TTCTTTCTGAAAAATGCAAGGCTTAAGGCAATGACAAACAAAGAGAAATGCTGAGAA 1680
Db 1621 TTCTTTCTGAAAAATGCAAGGCTTAAGGCAATGACAAACAAAGAGAAATGCTGAGAA 1680
QY 1681 ATTGGCAGCTGAGACAAAGCAATCTGAAATTAATTTTCCMAAAGTCTTTTATGTGAT 1740
Db 1681 ATTGGCAGCTGAGACAAAGCAATCTGAAATTAATTTTCCMAAAGTCTTTTATGTGAT 1740
QY 1741 ATAGTGTCAAGATTTGAAGAGCTATTTTATATGTTGCAATCTGCAACATCTTTC 1800
Db 1741 ATAGTGTCAAGATTTGAAGAGCTATTTTATATGTTGCAATCTGCAACATCTTTC 1800
QY 1801 GGAAGACAGCCAGGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
Db 1801 GGAAGACAGCCAGGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
QY 1861 TTTATCCCATATATTTAAATCAAGAAAAATGTGTATATCTTTAAGATTTTGATCA 1920
Db 1861 TTTATCCCATATATTTAAATCAAGAAAAATGTGTATATCTTTAAGATTTTGATCA 1920
QY 1921 ATACTTATATGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 ATACTTATATGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980

```


Db 1321 TCACAGCCACGCGCAACAAACACACACAAACATTGGAAATATTATCTCACTCA 1380
QY 1381 CGTTTAAATATACATCTTATTATTTTCTAGTAGAAGAACTACAAATCAGCCTTCA 1440
Db 1381 CGTTTAAATATACATCTTATTATTTTCTAGTAGAAGAACTACAAATCAGCCTTCA 1440
QY 1441 CATTATATACAGTTTAAATAGCCTTCTGAAAGTTACCTGTTCTCTCACCTGAGTTAT 1500
Db 1441 CATTATATACAGTTTAAATAGCCTTCTGAAAGTTACCTGTTCTCTCACCTGAGTTAT 1500
QY 1501 TTTTCTCCGCACTTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
Db 1501 TTTTCTCCGCACTTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
QY 1561 TTTTACATATTTGGGTCCAACTTCAATATATATATATATATATATATATATATAT 1620
Db 1561 TTTTACATATTTGGGTCCAACTTCAATATATATATATATATATATATATATATAT 1620
QY 1621 TTTCTCTTCAAGAAATAGCAAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 1680
Db 1621 TTTCTCTTCAAGAAATAGCAAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 1680
QY 1681 ATTGCACTGAGACAGCAATCTGAATTAATTTGCAAAAGTTCTTTTATGTCAT 1740
Db 1681 ATTGCACTGAGACAGCAATCTGAATTAATTTGCAAAAGTTCTTTTATGTCAT 1740
QY 1741 ATAGTGTCAAGATTTTGAAGAGTATTTTCTTAAATGTTGCACTAGCACTGTCAT 1800
Db 1741 ATAGTGTCAAGATTTTGAAGAGTATTTTCTTAAATGTTGCACTAGCACTGTCAT 1800
QY 1801 GGAAGACACAGCCAGAGAGATGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
Db 1801 GGAAGACACAGCCAGAGAGATGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
QY 1861 TTTATCCCATATTTTAAATTCAGAAATTTGTTTATCTTGAATTTTGTATCA 1920
Db 1861 TTTATCCCATATTTTAAATTCAGAAATTTGTTTATCTTGAATTTTGTATCA 1920
QY 1921 ATACTTATGATCTATGTCATGCTCTCTGGAATTAATTAAGCAACCAATATGATCTG 1980
Db 1921 ATACTTATGATCTATGTCATGCTCTCTGGAATTAATTAAGCAACCAATATGATCTG 1980
QY 1981 TAAACCAATCAACATATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
Db 1981 TAAACCAATCAACATATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
QY 2041 AGAAG 2091
Db 2041 AGAAG 2091

RESULT 3
AX017611 2411 bp DNA linear PART 07-SEP-2000
LOCUS Sequence 175 from Patent WO947655.
DEFINITION AX017611
ACCESSION AX017611 GI:10042337
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Schmitz,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pillarsky,C.
Human nucleic acid sequences from normal breast tissue
Patent: WO 947655-A 175 23-SEP-1999;
SCHEMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN
(DE); PILLARSKY CHRISTIAN (DE)
Location/Qualifiers
1. 2411
/organism="Homo sapiens"

FEATURES
source

ORIGIN
Query Match 97.4%; Score 2036; DB 6; Length 2411;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2031; Conservative 0; Mismatches 10; Indels 19; Gaps 2;
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

QY 1 AAGAGACAGCTATTAACCTGACAGTTAATTAAGACGTAATGTTTCAATGTTTATTTGTTA 60
Db 302 AAGAGACAGCTATTAACCTGACAGTTAATTAAGACGTAATGTTTCAATGTTTATTTGTTA 361
QY 61 AAGAGGTGAATAGGCTTCAAGCATGTAATATCTTCATGTTGCCCCG----- 111
Db 362 AAGAGGTGAATAGGCTTCAAGCATGTAATATCTTCATGTTTCCCCGACACATAC 421
QY 112 -----CGCTTTTGTCTTTCAGGTAGACCTTTTAAATGACAACTAATCTAGG 164
Db 422 ACAACACACATTTTGTCTTTCAGGTAGACCTTTTAAATGACAACTAATCTAGG 481
QY 165 CATTTCGTAACCTTGTCTTCAATCAATTAATCAATTAATTAATTAATTAATTAATTA 224
Db 482 CATTTCGTAACCTTGTCTTCAATCAATTAATCAATTAATTAATTAATTAATTAATTA 541
QY 225 TACTCTCATACCCCGTGTACTCAAAATCTCTACTGATGAATTAATGCTTTAAGTAAT 284
Db 542 TACTCTCATACCCCGTGTACTCAAAATCTCTACTGATGAATTAATGCTTTAAGTAAT 601
QY 285 TCACTGCCAAGAGAACTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 344
Db 602 TCACTGCCAAGAGAACTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 661
QY 345 AGCCATGATTTTATTTGTTGATGATGCTGTGACACAGCCATTTCAATAGATGA 404
Db 662 AGCCATGATTTTATTTGTTGATGATGCTGTGACACAGCCATTTCAATAGATGA 721
QY 405 GCTGTATATTTTCCAAAGATTAATGACATGCAAAAGTTTCAATTAATTAATTAATTA 464
Db 722 GCTGTATATTTTCCAAAGATTAATGACATGCAAAAGTTTCAATTAATTAATTAATTA 781
QY 465 TTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
Db 782 TTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 841
QY 525 TCCAAATACAAATTTGAAATCGTTGAAATAGCTGATTAATTTTCAGAAATGAATTTTC 864
Db 842 TCCAAATACAAATTTGAAATCGTTGAAATAGCTGATTAATTTTCAGAAATGAATTTTC 901
QY 585 ATTAATGAATCTGTTCCCTAGAGGCAATTTTCCCTTTCTGGAATTTAGCAATG 644
Db 902 ATTAATGAATCTGTTCCCTAGAGGCAATTTTCCCTTTCTGGAATTTAGCAATG 961
QY 645 TTAGAGAGAAATAGCTATGAAAGAAAGGAGAAAGGAGAAAGGAGAAAGGTTAAAA 704
Db 962 TTAGAGAGAAATAGCTATGAAAGAAAGGAGAAAGGAGAAAGGAGAAAGGTTAAAA 1021
QY 705 GTAAGTCTCAGACCTTGAAGCTAATCCCTTGTCTGAAATATTTTGAAGACAGCTCAG 764
Db 1022 GTAAGTCTCAGACCTTGAAGCTAATCCCTTGTCTGAAATATTTTGAAGACAGCTCAG 1081
QY 765 TTGCTGAAATCTAGTTTGTCAATCTTCAATTTTGAAGAGAGATTTTCTGACTGCA 824
Db 1082 TTGCTGAAATCTAGTTTGTCAATCTTCAATTTTGAAGAGAGATTTTCTGACTGCA 1141
QY 825 ATGACGTGAATGTAATTTTATTTTATTAATCTGTAAGAAAGCTGACTGTAAGAAATGA 884
Db 1142 ATGACGTGAATGTAATTTTATTTTATTAATCTGTAAGAAAGCTGACTGTAAGAAATGA 1201
QY 885 TAAATATTTGAGGTTTCTGTCATATCTGCTTGCATGTCAGAAAGAGAGAAATAGA 944
Db 1202 TAAATATTTGAGGTTTCTGTCATATCTGCTTGCATGTCAGAAAGAGAGAAATAGA 1261
QY 945 AAATGTAATCTCCCAATCCAGATGAAACCCAGGGTGAAGCAATTTCTATGTAAGTT 1004

```
Db 1262 AAAAGTAATCTCCACATCCAGATCGAAGCCCAAGGGGTAGGCAATTCATCTAGT 1321
Qy 1005 TTGGACATGAAGTTGGTGCATCTTGGTTATAGCTGGCTCACTGTTAAACCTCT 1064
Db 1322 TTGGACATGAAGTTGGTGCATCTTGGTTATAGCTGGCTCACTGTTAAACCTCT 1381
Qy 1065 GGCCTATAGTCTCTTCAATCTTATTAAGACGATCGAAGCACTTGCTGGACAGG 1124
Db 1382 GGCCTATAGTCTCTTCAATCTTATTAAGACGATCGAAGCACTTGCTGGACAGG 1441
Qy 1125 CTCTTACTGTAACATTTTAAAGCAGTACTGTTGGTTAAACACTTTGACCAATAG 1184
Db 1442 CTCTTACTGTAACATTTTAAAGCAGTACTGTTGGTTAAACACTTTGACCAATAG 1501
Qy 1185 TTCTGAGGCAACGAGACATGACTATTTAAAGAGCTTTCCAGCATCACTTAC 1244
Db 1502 TTCTGAGGCAACGAGACATGACTATTTAAAGAGAGCTTTCCAGCATCACTTAC 1561
Qy 1245 ATCCCAAACTAAAAAGATCAACTCTTCCAACTGAGAAAAGACTCTGGCTTGAATGA 1304
Db 1562 ATCCCAAACTAAAAAGATCAACTCTTCCAACTGAGAAAAGACTCTGGCTTGAATGA 1621
Qy 1305 AACTTACAGCAGAGAGTCAAGGCGGCAACGCAACGACAAACAACAACTTTGAA 1364
Db 1622 AACTTACAGCAGAGAGTCAAGGCGGCAACGCAACGACAAACAACAACTTTGAA 1681
Qy 1365 TATTAATCTCAACCTACGTTTAAATATATATCTTATTTTCTAGTAGAAGAACTAC 1424
Db 1682 TATTAATCTCAACCTACGTTTAAATATATATCTTATTTTCTAGTAGAAGAACTAC 1741
Qy 1425 AATAGAGCTCTTCAACATTTATATACAGTTTAAATAGCTCTGCAAGTACTGTTCT 1484
Db 1742 AATAGAGCTCTTCAACATTTATATACAGTTTAAATAGCTCTGCAAGTACTGTTCT 1801
Qy 1485 CTACCTGAGATTTTCTCTCCCACTGGCCCTGTTCTCCCTCTCTCTCC 1544
Db 1802 CTACCTGAGATTTTCTCTCCCACTGGCCCTGTTCTCCCTCTCTCTCC 1861
Qy 1545 TTTCGAAAGGAAATTTTAAATATATTTGGTCCAACTCAATATATATATATATAC 1604
Db 1862 TTTCGAAAGGAAATTTTAAATATATTTGGTCCAACTCAATATATATATATAC 1921
Qy 1605 ATTTAAAGCATTTAATCTCTCTTCTAGAAAAATGCAAGGCTAAGGCAATAGACAAA 1664
Db 1922 ATTTAAAGCATTTAATCTCTCTTCTAGAAAAATGCAAGGCTAAGGCAATAGACAAA 1981
Qy 1665 AAGAGAAATGCTGAGAAATTTGCACTGAGACAGCAATCTGATTAATTTTGGCAAA 1724
Db 1982 AAGAGAAATGCTGAGAAATTTGCACTGAGACAGCAATCTGATTAATTTTGGCAAA 2041
Qy 1725 GTTCTTTTATGATATATAGTGTGAGATTTGAGAGACTATTTTATATGTTGCA 1784
Db 2042 GTTCTTTTATGATATATAGTGTGAGATTTGAGAGACTATTTTATATGTTGCA 2101
Qy 1785 CTAGCAACTCATCTTGGAGAGACAGCCAGAGAGATGAGAGTGAAGGTTATTA 1844
Db 2102 CTAGCAACTCATCTTGGAGAGACAGCCAGAGAGATGAGAGTGAAGGTTATTA 2161
Qy 1845 AATCATTTTGTAAAGATTTATGCCATATATTTTAAATCAAGAAATTTGTTATCTT 1904
Db 2162 AATCATTTTGTAAAGATTTATGCCATATATTTTAAATCAAGAAATTTGTTATCTT 2221
Qy 1905 TAGAATTTTGTATCAATCTTATATGATATGATCACTGCTTCTGATTAATTAAGC 1964
Db 2222 TAGAATTTTGTATCAATCTTATATGATATGATCACTGCTTCTGATTAATTAAGC 2281
Qy 1965 ACCAAATATGATCTGTAAACCAATCAACATATATATATATATATATATATAC 2024
Db 2282 ACCAAATATGATCTGTAAACCAATCAACATATATATATATATATATATAC 2341
Qy 2025 AGCCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2081
```

```
Db 2342 AGCCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2401
Qy 2082 GGGGGGAGGT 2091
Db 2402 GGGGGGAGGT 2411

RESULT 4
BD135230
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2411)
Speft T., Hintzman, B., Shmidt, A., Pirarski, C., Duhl, E. and
Rosenthal, A.
Human nucleic acid sequence originating in normal mammary tissue
Patent: JP 2002506639-A 77 05-MAR-2002;
METAGEN GESELISCHAFT FUER GENOME FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002506639-A/77
PD 05-MAR-2002
PF 19-MAR-1998 JP 2000536838
PR 20-MAR-1998 DE 198 13 835.0
PI THOMAS SPEFT, BERNH HINTZMAN, ARMIN SHOWITT, CHRISTIAN PIRARSKI,
PI EDGAR DUHL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K46/00, A61P35/00, A61P43/00, A61P43/00, C07K14/47,
PC C07K16/18
PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//A61K38/00, PC
C12N15/00,
PC C12N5/00, A61K37/02
CC Human nucleic acid sequence originating in normal mammary CC

FH Key 1. 2411 Location/Qualifiers
FT source 1. 2411 /organism='Homo sapiens (human)'.

FEATURES
source
1. 2411
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 97.4%; Score 2036; DB 6; Length 2411;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2081; Conservative 0; Mismatches 10; Indels 19; Gaps 2;

1 AAGAGACAGCTATTAAGTCAAGTAAATTAAGACGATGTTCCATGTTATTTGTTA 60
302 AAGAGACAGCTATTAAGTCAAGTAAATTAAGACGATGTTCCATGTTATTTGTTA 361
61 AAGAGTGAATAGCTTCAAGCATGATATATCTTCATCTTCCCGC----- 111
362 AAGAGTGAATAGCTTCAAGCATGATATATCTTCATCTTCCCGC----- 421
112 -----CGTTTGTCTTCTTCAAGTGAACCTTTTAAATGAGAACTAAGG 164
422 AAGAGTGAATAGCTTCAAGCATGATATATCTTCATCTTCCCGC----- 481
165 CATTGATTAAGTCTTCAAGTAAATTAAGTGAATGAGAACTTTGTTGCCC 224
482 CATTGATTAAGTCTTCAAGTAAATTAAGTGAATGAGAACTTTGTTGCCC 541
225 TACTTCCATACCCCGTGAATCAATCTTCAAGTGAATGAGAACTTTGTTGCCC 284
542 TACTTCCATACCCCGTGAATCAATCTTCAAGTGAATGAGAACTTTGTTGCCC 601
```

QY	285	TCAGTGC	CAAGGAA	CACTTGG	TGA	TA	AAATTT	TAATTTT	TTTAT	CTTTT	TAT	CTTTT	TAC	344
Db	602	TCAGTGC	CAAGGAA	CACTTGG	TGA	TA	AAATTT	TAATTTT	TTTAT	CTTTT	TAT	CTTTT	TAC	661
QY	345	AGCCATG	GAATTT	TAATTTG	GTG	TG	TGCTGT	GA	CA	AGCCAT	TTCA	TA	AGAT	404
Db	662	AGCCATG	GAATTT	TAATTTG	GTG	TG	TGCTGT	GA	CA	AGCCAT	TTCA	TA	AGAT	721
QY	405	GCTGT	TAATTT	TTTTC	CA	AGAT	TA	AGCA	AGCA	AACTT	TC	AT	TA	464
Db	722	GCTGT	TAATTT	TTTTC	CA	AGAT	TA	AGCA	AGCA	AACTT	TC	AT	TA	781
QY	465	TTAACAA	TAATTA	TAATA	CTAT	TA	AGCA	TTCCCT	CT	AG	TTTTT	TGCC	AA	524
Db	782	TTAACAA	TAATTA	TAATA	CTAT	TA	AGCA	TTCCCT	CT	AG	TTTTT	TGCC	AA	841
QY	525	TCCAATA	CAAA	TTTG	A	AT	CGTT	GA	AAAA	AG	TA	TA	TTT	584
Db	842	TCCAATA	CAAA	TTTG	A	AT	CGTT	GA	AAAA	AG	TA	TA	TTT	901
QY	585	ATTAT	TTGA	AC	TG	T	CCCT	AG	CA	AGG	CA	TTTT	CC	644
Db	902	ATTAT	TTGA	AC	TG	T	CCCT	AG	CA	AGG	CA	TTTT	CC	961
QY	645	TTAGAGA	GAA	TAG	CA	TG	AA	AA	GA	AGG	GA	AA	GG	704
Db	962	TTAGAGA	GAA	TAG	CA	TG	AA	AA	GA	AGG	GA	AA	GG	1021
QY	705	GTAAG	TG	CT	GA	CC	TA	GA	AC	GT	TA	CC	CT	764
Db	1022	GTAAG	TG	CT	GA	CC	TA	GA	AC	GT	TA	CC	CT	1081
QY	765	TTGGT	TGA	AC	TG	AT	TT	GT	CA	TT	TC	CA	TA	824
Db	1082	TTGGT	TGA	AC	TG	AT	TT	GT	CA	TT	TC	CA	TA	1141
QY	825	ATGCA	G	CT	AG	AT	GT	AA	ATTT	TA	TT	TA	TC	884
Db	1142	ATGCA	G	CT	AG	AT	GT	AA	ATTT	TA	TT	TA	TC	1201
QY	885	TAAAT	T	T	G	A	G	G	G	T	T	C	C	944
Db	1202	TAAAT	T	T	G	A	G	G	G	T	T	C	C	1261
QY	945	AAATG	T	A	T	A	T	C	C	A	A	T	C	1004
Db	1262	AAATG	T	A	T	A	T	C	C	A	A	T	C	1321
QY	1005	TTGGA	C	A	T	A	G	T	T	G	T	G	C	1064
Db	1322	TTGGA	C	A	T	A	G	T	T	G	T	G	C	1381
QY	1065	GCGT	A	T	A	G	T	C	T	T	C	A	T	1124
Db	1382	GCGT	A	T	A	G	T	C	T	T	C	A	T	1441
QY	1125	CTCTT	A	G	T	A	C	A	TTT	B	G	A	C	1184
Db	1442	CTCTT	A	G	T	A	C	A	TTT	B	G	A	C	1501
QY	1185	TTCTG	A	G	G	A	A	A	A	T	G	A	A	1244
Db	1502	TTCTG	A	G	G	A	A	A	A	T	G	A	A	1561
QY	1245	ATCC	A	A	A	A	A	A	A	G	A	T	C	1304
Db	1562	ATCC	A	A	A	A	A	A	A	G	A	T	C	1621
QY	1305	AACTT	A	C	A	G	A	G	A	G	A	T	C	1364
Db	1622	AACTT	A	C	A	G	A	G	A	G	A	T	C	1681
QY	1365	TATAT	T	T	T	C	A	C	T	G	T	T	T	1422

Db	1682	TATATTCTGCACTCAGCTTTTAAATACATCTTTATTTTCTAGTAGAAGAACTAC	1741		
QY	1425	AAATCAGCCTCTTCAACATTTATATACAGTTTAAATAGCCTCTTGCAAGTTACTTGTTCT	1484		
Db	1742	AAATCAGCCTCTTCAACATTTATATACAGTTTAAATAGCCTCTTGCAAGTTACTTGTTCT	1801		
QY	1485	CTCACTGAGATATTTTTTCCGCCACCTGGCCCTGTGCTCCCTTCCTCTCTCCG	1544		
Db	1802	CTCACTGAGATATTTTTTCCGCCACCTGGCCCTGTGCTCCCTTCCTCTCTCCG	1861		
QY	1545	TTTGCAAGAGAAATTTTAAACATATTTGGGTCCAACTTCAATATATATATATATAC	1604		
Db	1862	TTTGCAAGAGAAATTTTAAACATATTTGGGTCCAACTTCAATATATATATATATAC	1921		
QY	1605	ATTAAAGCATTTTAACTTCTCTTCTTGAAAAATGCAAGGCTTAAAGCATAGACAAAACA	1664		
Db	1922	ATTAAAGCATTTTAACTTCTCTTCTTGAAAAATGCAAGGCTTAAAGCATAGACAAAACA	1981		
QY	1665	AGGAATATGCTGGAATTTGCAATTTGCACTGAGACAAGCAATCTGAATTAATTTGCCAAA	1724		
Db	1982	AGGAATATGCTGGAATTTGCAATTTGCACTGAGACAAGCAATCTGAATTAATTTGCCAAA	2041		
QY	1725	GTTCCTTTTATGTCATATAGTGTGAGATTGAAAGAGCTATTTTTTTTAAATGTTGCA	1784		
Db	2042	GTTCCTTTTATGTCATATAGTGTGAGATTGAAAGAGCTATTTTTTTTAAATGTTGCA	2101		
QY	1785	CTAGCACTATCTCTTGGAAGACACAGCCAGAGAAATGAAGTGAAGTGAAGTTTATA	1844		
Db	2102	CTAGCACTATCTCTTGGAAGACACAGCCAGAGAAATGAAGTGAAGTGAAGTTTATA	2161		
QY	1845	AATCATTTTGTAAGCATTTTATCCCATATATTTTAAATTCAGAAAAATTTGTTTACTT	1904		
Db	2162	AATCATTTTGTAAGCATTTTATCCCATATATTTTAAATTCAGAAAAATTTGTTTACTT	2221		
QY	1905	TAGATTTTGTATTCATACTTTATAGTACATATGCACTCATGCTCTGAGATTAATAAGC	1964		
Db	2222	TAGATTTTGTATTCATACTTTATAGTACATATGCACTCATGCTCTGAGATTAATAAGC	2281		
QY	1965	ACCAATATGATCTGTACCAACATACACATATTAATTAATATATATCTATATATAC	2024		
Db	2282	ACCAATATGATCTGTACCAACATACACATATTAATTAATATATATCTATATATAC	2341		
QY	2025	AGCCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2081		
Db	2342	AGCCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2401		
QY	2082	GGGGGGGAGGT 2091			
Db	2402	GGGGGGGAGGT 2411			
RESULT 5	BD218591	3674 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD218591				
DEFINITION	71 human secretory proteins.				
ACCESSION	BD218591				
VERSION	BD218591.1				
KEYWORDS	JP 2002520050-A/72.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (baes 1 to 3674)				
	Ruben,S.M., Komatsoulis,G., Duan,R.D., Rosen,C.A., Moore,P.A.,				
	Shi,Y., Lafleur,D.W., Ebner,R., Olsen,H.S., Brewer,L.A.,				
	Florence,K.A., Young,P.E., Mucenski,M., Endrease,G.A. and				
	Sopeck,D.R.				
	71 human secretory proteins				
	Patent: JP 2002520050-A 72 09-JUL-2002;				
	HUMAN GENOME SCIENCES INC				
	OS Homo sapiens (human)				
	PN JP 2002520050-A/72				
TITLE	71 human secretory proteins				
JOURNAL	HUMAN GENOME SCIENCES INC				
COMMENT	OS Homo sapiens (human)				
	PN JP 2002520050-A/72				

PD 09-JUL-2002
PF 14-JUL-1999 JP 2000560238
PR 15-JUL-1998 US 60/092921,15-JUL-1998 US 60/092922 PR
15-JUL-1998 US 60/092956
PI STEVEN M RUBEN, GEORGE KOMATSOUJIS, ROXANNE
D DUAN, CRAIG A ROSEN,
PI PAUL A MOORE, YANQU SHI, DAVID W LAFLEUR, REINHARD EBNER, HENRIK
PI S OLSEN,
PI LAURIE A BREWER, KIMBERLY A FLORENCE, PAUL E YOUNG, MICHAEL PI
MUCENSKI,
PI GREGORY A ENDESS, DANIEL R SOPPEI
PC C12N15/09, C07H21/02, C07H21/04, C07K16/47, C07K16/18, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, G01N33/50, G01N33/68//C12Q1/68, PC
C12N15/00,
PC C12N5/00
CC 71 human secretory proteins
FH Key Location/Qualifiers
FT source 1.3674
/organism="Homo sapiens (human)".
Location/Qualifiers
Source 1.3674
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"

Query Match 95.8%; Score 2003.8; DB 6; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2034; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

ORIGIN

1 AAGAGACAGCTAATCACTTCAAGTAAATTAAGAGAGTATGTCATGTTATTTGTA 60
1617 AAGAGACAGCTAATCACTTCAAGTAAATTAAGAGAGTATGTCATGTTATTTGTA 1676
61 AAGAGAGTGAATAGCTTCAAGTAAATTAAGTAAATCTTCCCTCCG-----111
1677 AAGAGAGTGAATAGCTTCAAGTAAATTAAGTAAATCTTCCCTCCGCAACATAC 1736
112 -----CGCTTTGTTCTTCTTCAGTAAACCTTTTAAAGCAGAACTACAG 164
1737 AACACACACTTTGTTCTTCTTCAGTAAACCTTTTAAAGCAGAACTACAG 1796
165 CATTCACTAATCTTCTTCAATCAATTAAGTCAATGATGAGAAACATTTTGCC 224
1797 CATTCACTAATCTTCTTCAATCAATTAAGTCAATGATGAGAAACATTTTGCC 1856
225 TACTCTCAATCCCGTCTCAATCTCTCACTGATGATGATGATGATGATGAT 284
1857 TACTCTCAATCCCGTCTCAATCTCTCACTGATGATGATGATGATGATGAT 1916
285 TCAGTCCAGAGAGAACTTGGTGAATTAATTTATTTTATTTTATCTTCA 344
1917 TCAGTCCAGAGAGAACTTGGTGAATTAATTTATTTTATTTTATTTTATCTTCA 1976
345 AGCCATGATTTTATTTGTTGATGATGATGATGATGATGATGATGATGATGAT 404
1977 AGCCATGATTTTATTTGTTGATGATGATGATGATGATGATGATGATGATGAT 2036
405 GGTGTTAATTTATTTTCAAGGATTAAGATGAGAAAGTTTCAATTAAGCTGGGCA 464
2037 GGTGTTAATTTATTTTCAAGGATTAAGATGAGAAAGTTTCAATTAAGCTGGGCA 2096
465 TTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
2097 TTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2156
525 TCCATTAATTAATTTGAGAACTGTTGAGAAAGCTGTTATTTTCAAGAAATGATTTTC 584
2157 TCCATTAATTAATTTGAGAACTGTTGAGAAAGCTGTTATTTTCAAGAAATGATTTTC 2216
585 ATTATTAATTAATTTCTCCCTAGAGGCAATTTCTCTTTCTGAGGATTTAGCAAGT 644

2217 ATTATTAATTAATTTCTCCCTAGAGGCAATTTCTCTTTCTGAGGATTTAGCAAGT 2276
645 TTAGAGAGAAATAGTCAATGAAAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 704
2277 TTAGAGAGAAATAGTCAATGAAAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2336
705 GTAAGTCTCAAGCTTAAGAAAGTAAATCCCTTTGTTAATTAATTTAAGAGAGCTCAGC 764
2337 GTAAGTCTCAAGCTTAAGAAAGTAAATCCCTTTGTTAATTAATTTAAGAGAGCTCAGC 2396
765 TTGTTGAAGAACTGATTTGTTGATCTTCCATATTTTTCAGAGAGATTTTTCGACTTGA 824
2397 TTGTTGAAGAACTGATTTGTTGATCTTCCATATTTTTCAGAGAGATTTTTCGACTTGA 2456
825 ATGACAGTATGATGATTAATTTTATTTTATCTCTGAGAAAGCTTGAATTAATTAAT 884
2457 ATGACAGTATGATGATTAATTTTATTTTATCTCTGAGAAAGCTTGAATTAATTAAT 2516
885 TAAATTTAGAGGTTTCTGTCATATGCTGATGCTGATGCTGATGCTGATGCTGAT 944
2517 TAAATTTAGAGGTTTCTGTCATATGCTGATGCTGATGCTGATGCTGATGCTGAT 2576
945 AATGTTATCTCAACATCAAGCATCGAAATCCCAAGGGTATGGCAATTTCTATGATGTT 1004
2577 AATGTTATCTCAACATCAAGCATCGAAATCCCAAGGGTATGGCAATTTCTATGATGTT 2636
1005 TTGACATGAAATTTGGTGCATCTGTTATGCTGCTCACTGCTCACTGCTCACTGCT 1064
2637 TTGACATGAAATTTGGTGCATCTGTTATGCTGCTCACTGCTCACTGCTCACTGCT 2696
2697 GGCTTATGCTCTTCACTCACTATTAAGACAGACATGACATGCTGCTCACTGCTCACT 2756
1125 CTCTTATGTTCAATTTAGAGAGTATGCTGTTGTTTAAAGCAGCTTTTCAAGAAATAG 1184
2757 CTCTTATGTTCAATTTAGAGAGTATGCTGTTGTTTAAAGCAGCTTTTCAAGAAATAG 2816
1185 TTCTGAGCAAGAGAGAGATGATGATTTTAAAGAAAGCTTTCCAGATCACTTAC 1244
2817 TTCTGAGCAAGAGAGAGATGATGATTTTAAAGAAAGCTTTCCAGATCACTTAC 2876
1245 ATCCCAAACTAAAGAGATCACTTCCATCTGAGAAAGCTCTGCTTTGATGTA 1304
2877 ATCCCAAACTAAAGAGATCACTTCCATCTGAGAAAGCTCTGCTTTGATGTA 2936
1305 AACTACAGAGAGAGTCAAGGCAAGGCAACAAAGCAAGCAAGCAAGCAAGCAAGT 1364
2937 AACTACAGAGAGAGTCAAGGCAAGGCAAGGCAACAAAGCAAGCAAGCAAGCAAGT 2996
1365 TATTATTTCACTCACTGTTTAAATTAATTAATTAATTTTCTAGTAGAAAGCTAC 1424
2997 TATTATTTCACTCACTGTTTAAATTAATTAATTAATTTTCTAGTAGAAAGCTAC 3056
1425 AATTCAGCTCTTCAACATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1484
3057 AATTCAGCTCTTCAACATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3116
1485 CTCACCTGAGATTTTCTTCCCACTTCCCTGCTTCTGCTGCTTCTGCTTCTGCT 1544
3117 CTCACCTGAGATTTTCTTCCCACTTCCCTGCTTCTGCTGCTTCTGCTTCTGCT 3176
1545 TTTCAGAGAGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1604
3177 TTTCAGAGAGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3236
1605 ATTAAGAGATTTAATTTCTTCTTGAAGAAATGCAAGGCTTAAGCATGACAAACAA 1664
3237 ATTAAGAGATTTAATTTCTTCTTGAAGAAATGCAAGGCTTAAGCATGACAAACAA 3296
1665 AGAGAAATGCTGAGAAATTTGCACTGAGAGCAAGCAATCTGAATTAATTTTCCAA 1724
3297 AGAGAAATGCTGAGAAATTTGCACTGAGAGCAAGCAATCTGAATTAATTTTCCAA 3356

	Db	1786	GTTCTTTTAAAGTCATATAGGTGAGATTGAAGAAGCATTTTTTTTAATGGTGCA	1786
	Qy	1785	CTAGCAACTCATTCTTCGGAGACACACGCCAGAGAGATGAGTAGAAGTGAAGGTTATA	1844
	Db	1845	CTAGCAACTCATTCTTCGGAGAGACACAGCGAGAGAAAGTAGAAGTGAAGGTTATA	3476
	Qy	1845	AATCCATTGTAGAGATTATCCCATATATTTTAAATCAAGAAAATTTGGTTATCTT	1904
	Db	3537	AATCCATTGTAGAGATTATCCCATATATTTTAAATCAAGAAAATTTGGTTATCTT	3536
	Qy	1905	TAGATTTTGTATTCATCTTATCTTATGTACTATGTGACTCATGCTTCTGGATTAATAAAC	1964
	Db	1965	ACCAAATATGTATCTGTACAACAATCACATCTTTATATTAATATATATATATATATAC	2024
	Qy	3537	ACCAAATATGTATCTGTACAACAATCACATCTTTATATTAATATATATATATATAC	3656
	Qy	2025	AGCCAAAAAAAAAAAAA 2041	
	Db	3657	AAAAAAAAAAAAAAAAA 3673	
RESULT 6				
LOCUS	HSMB05729	5683 bp	mRNA	linear PRI 16-JUN-2003
DEFINITION	Homo sapiens mRNA; CDNA DKFZp686g1211 (from clone DKFZp686g1211); complete cds.			
ACCESSION	BX37427			
VERSION	BX37427.1	GI:31873355		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
JOURNAL	Mammalia; Eutheria; Primates; Carnivora; Felidae; Mustelidae; Mammalia; Eutheria; Primates; Carnivora; Felidae; Mustelidae; Homo. 1 (bases 1 to 5683)			
REFERENCE	Bloecher,H., Boecker,M., Meves,H.W., Well,B., Amlid,C., Osanger,A., Poldo,G., Han,M. and Wiemann,S.			
AUTHORS	Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY			
TITLE	Clohe from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;			
COMMENT	Research by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp686g1211) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cdna/. Location/Qualifiers 1..5683 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /map="ig23" /clone="DKFZp686g1211" /tissue_type="human cervix" /clone_1kb=686 (synonym: hicc3). Vector pSport1_Sfi; host DH10B; sites SfiI + SfiIB /dev_stage="adult" 1..5683 /gene="DKFZp686g1211" 83..628 /gene="DKFZp686g1211" /note="G protein signaling regulator RGSS" /codon_start=1 /product="hypothetical protein" /protein_id="CAD97669.1"			

Query Match	Best Local Similarity	98.7%	Score 2001.2	DB 9	Length 5683
Matches 2032	Conservative	0	Mismatches	8	Indels 16
Gaps	1				
polya_signal	5646. .5651				
polya_site	/gene="DKFZp686g1211"				
ORIGIN	/gene="DKFZp686g1211"				
Query Match	95.7%	Score 2001.2	DB 9	Length 5683	
Best Local Similarity	98.8%	Pred. No. 0			
Matches 2032	Conservative	0	Mismatches	8	Indels 16
Gaps	1				
1	AAGAGACAGACTATTAACTCCACAGTTAATTAAAGACGTAATGTTCCATGTTATTGTTA	60			
3628	AAGAGACAGACTATTAACTCCACAGTTAATTAAAGAGTAATGTTCCATGTTATTGTTA	3687			
61	AAGAGAGTGAATAGCCCTTCAAGATGTAATCTTCATCTTCCCGC-----	111			
3688	AAGAGAGTGAATAGCCCTTCAAGATGTAATCTTCATCTTCCCGC-----	3747			
112	-----CGCTTTTGTTCCTTCAAGTAAACACCTTTTAAATGCAACTAAGT	164			
3748	ACACACACACTTTTGTTCCTTCAAGTAAACACCTTTTAAATGCAACTAAGT	3807			
165	CATTTCAGTACTTTGCTTCAATCAATAAGTCAATGTAAGTGAACAATTTGTGCC	224			
3808	CATTTCAGTACTTTGCTTCAATCAATAAGTCAATGTAAGTGAACAATTTGTGCC	3867			
225	TACTCTCCAAACCCCGTGAATCAATCTCTCACTGTAATGTAATGCTTAAAT	284			
3868	TACTCTCCAAACCCCGTGAATCAATCTCTCACTGTAATGTAATGCTTAAAT	3927			
285	TCAGTGCACAGAGAACTTGGTGAATAATATTATTATTTTATTCCTTTACA	344			
3928	TCAGTGCACAGAGAACTTGGTGAATAATATTATTATTTTATTCCTTTACA	3987			
345	AGCATGAGTTTATTGTTGATGTGCTGTGTACACAGCCATTCAATAGATGA	404			
3988	AGCATGAGTTTATTGTTGATGTGCTGTGTGTACACAGCCATTCAATAGATGA	4047			
405	GCTGTATTATTTTCCCAAGAGTAATAGATCAACAAAGTTCAATTAACCTGGCCA	464			
4048	GCTGTATTATTTTCCCAAGAGTAATAGATCAACAAAGTTCAATTAACCTGGCCA	4107			
465	TTACAAATAATTAATACTAATAGCATTTCCCTCTAGCTTTTGGCCAACTGGCTA	524			
4108	TTACAAATAATTAATACTAATAGCATTTCCCTCTAGCTTTTGGCCAACTGGCTA	4167			
525	TCCATTAACAATTTGAGATCGTTGAAAAAGCTAGTTAATTTCAAGAAATGATTTTC	584			
4168	TCCATTAACAATTTGAGATCGTTGAAAAAGCTAGTTAATTTCAAGAAATGATTTTC	4227			
585	ATTATTGAACTGTTCTCCCTAGCAGGCCATTTTCCCTTTTCCGGGAGTTAGCAAT	644			
4228	ATTATTGAACTGTTCTCCCTAGCAGGCCATTTTCCCTTTTCCGGGAGTTAGCAAT	4287			
645	TTAGAGAGAAATAGTCATGAAAAAGAAAGGAAAGGGAAGAGGAAAGGTTAAAA	704			
4288	TTAGAGAGAAATAGTCATGAAAAAGAAAGGAAAGGGAAGAGGAAAGGTTAAAA	4347			
705	GTAATGCTCAGACCTATGAAAGCTAATCCCTTGTATAAATATTAAAGAGCTCAGC	764			
4348	GTAATGCTCAGACCTATGAAAGCTAATCCCTTGTATAAATATTAAAGAGCTCAGC	4407			
765	TTGATGGAACCTGATTTGTATCTTCATATTTGACAGAAAGTATTTTCTGACTGCA	824			
4408	TTGATGGAACCTGATTTGTATCTTCATATTTGACAGAAAGTATTTTCTGACTGCA	4467			
825	ATGCACTGAGATGTAATTTTATTTTATCTTCAAGAAAGCTGACAGAAATGAA	884			

Db	4468	ATGCAGCTAATGTAATAATTTTATTATTATCATACTAGAAAAGCCTTGACTGAAAAATTCGA	4522
Qy	885	TAAATATTGAGGGTTTCCTGTCATATCTG3CTTGACATGTCGCGAAGAAACAGAGATAGA	944
Db	4528	TAAATATTGAGGGTTTCCTGTCATATCTG3CTTGACATGTCGCGAAGAAACAGAGATAGA	4587
Qy	945	AAATGTAAATCCCAACATCCAGAGATGAAACCCAAAGGGGTAGGCAATTCTATGATAGGT	1004
Db	4588	AAATGTAAATCCCAACATCCAGAGATGAAACCCAAAGGGGTAGGCAATTCTATGATAGGT	4647
Qy	1005	TTGCACATGAAGTTTGGTGACATCTTGGTTATGCTGGCTCACTGCTATTAAACCTCTCT	1064
Db	4648	TTGCACATGAAGTTTGGTGACATCTTGGTTATGCTGGCTCACTGCTATTAAACCTCTCT	4707
Qy	1065	GGCTTAATAGTCTCTTCACTTCTATTAGACAAAGATATCGAAACATCTGTGCGACAGG	1124
Db	4708	GGCTTAATAGTCTCTTCACTTCTATTAGACAAAGATATCGAAACATCTGTGCGACAGG	4767
Qy	1125	CTCTTATGTTAAACATTTTAGAGCTACTGTTTGTTGTTAAACACACTTTTCCAAATAGG	1184
Db	4768	CTCTTATGTTAAACATTTTAGAGCTACTGTTTGTTGTTAAACACACTTTTCCAAATAGG	4827
Qy	1185	TTCTGAGCGCAACGAGAGCAATGACATTTTAAAGAAAGCTTTCGACATCACTTACAC	1244
Db	4828	TTCTGAGCGCAACGAGAGCAATGACATTTTAAAGAAAGCTTTCGACATCACTTACAC	4887
Qy	1245	ATCCCAAAACCTAAAAAAGTCAACTCTTCCAACTGAGAAAAGACTCTGGCTTTGAATGA	1304
Db	4888	ATCCCAAAACCTAAAAAAGTCAACTCTTCCAACTGAGAAAAGACTCTGGCTTTGAATGA	4947
Qy	1305	AACTTACAGCAGAGAGTCACAGGCGCACGGCAACACACACACACACAAATTTGGAA	1364
Db	4948	AACTTACAGCAGAGAGTCACAGGCGCACGGCAACACACACACACACAAATTTGGAA	5007
Qy	1365	TATATTCTCACTCAGGTTTAAATATATACATCTATATTTTCTATGATAGAAATAC	1424
Db	5008	TATATTCTCACTCAGGTTTAAATATATACATCTATATTTTCTATGATAGAAATAC	5067
Qy	1425	AAATCAGCGCTTCGACACTTATATATACAGTTTAAAGCCCTTGCAAGTTACTTGTCT	1484
Db	5068	AAATCAGCGCTTCGACACTTATATATACAGTTTAAAGCCCTTGCAAGTTACTTGTCT	5127
Qy	1485	CTCACCTGAGTATTTTTTCTCTCCCACTTGCGCCCTGTCCGCCCTCCTCTCTCCC	1544
Db	5128	CTCACCTGAGTATTTTTTCTCTCCCACTTGCGCCCTGTCCGCCCTCCTCTCTCCC	5187
Qy	1545	TTTCCAGAGAGAAATATTAAATATTTAGGCTCCAACTTCATATGTAATTAATTAATAC	1604
Db	5188	TTTCCAGAGAGAAATATTAAATATTTAGGCTCCAACTTCATATGTAATTAATTAATAC	5247
Qy	1605	ATTAAAGCATTTAACTTCTCTTGTAGAAAAATGACAGGCTTAAAGCATAGACAAAACAA	1664
Db	5248	ATTAAAGCATTTAACTTCTCTTGTAGAAAAATGACAGGCTTAAAGCATAGACAAAACAA	5307
Qy	1665	AGAGAAATGCGAGAAATTTGCCACTGAGAACAGCAATCTGAATTAATTTTGGCAAAA	1724
Db	5308	AGAGAAATGCGAGAAATTTGCCACTGAGAACAGCAATCTGAATTAATTTTGGCAAAA	5367
Qy	1725	GTTCTTTTATGTCAATATAGTGTGACGATTTGAAGAGCTATTTTTTTTAAATGTTGCAA	1784
Db	5368	GTTCTTTTATGTCAATATAGTGTGACGATTTGAAGAGCTATTTTTTTTAAATGTTGCAA	5427
Qy	1785	CTAGCAACTCATCTTTCGGAAGACACAGCAAGAGAAATGAATAGAGGAAGTTATA	1844
Db	5428	CTAGCAACTCATCTTTCGGAAGACACAGCAAGAGAAATGAATAGAGGAAGTTATA	5487
Qy	1845	AATCATTTGTAGACATTTATCCCATATATTTTAAATTCAGAAAAAATGTGTTATCTT	1904
Db	5488	AATCATTTGTAGACATTTATCCCATATATTTTAAATTCAGAAAAAATGTGTTATCTT	5547
Qy	1905	TAGAAATTTGTATTCATATCTTTATATGTAATGTAATCACTCACTCTCTGATTAATAAAGC	1966
Db	5548	TAGAAATTTGTATTCATATCTTTATATGTAATGTAATCACTCACTCTCTGATTAATAAAGC	5607

QY 1365 ACCGAAATATCTATCTGTAAACCAAGATACAGCATTTATTTAAATATATATCTCTTAATAC 2024
Db 5608 ACCGAAATATGTATCTGTAAACCAAGATACAGCATTTATTTAAATATATATCTCTTAATAAA 5667
QY 2025 AGCCGAAAAAAAAAAAA 2040
Db 5668 AAAAAAAAAAAAAACA 5683

RESULT	7
LOCUS	AC031977
DEFINITION	AC031977 191699 bp DNA linear HTG_12-APR-2001
ACCSSION	Homo sapiens chromosome 1 clone RP11-288018, WORKING DRAFT SEQUENCE, 3 unordered pieces.
VERSION	AC031977
KEYWORDS	AC031977.7 GI:13194952
SOURCE	HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULTOP; HTGS_ACTIVEFIN.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 191699)
Abola, A.P., Bruno, D., Com, L., Dela Rosa, M., Faulkner, D.,
Pedersjeld, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
MacI, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M.,
Mochouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D.,
Southwick, A.N., Webb, C., Wilhelmy, J., Yu, S. and Davis, R. W.
Unpublished
2 (bases 1 to 191699)
Abola, A.P., Bruno, D., Com, L., Dela Rosa, M., Faulkner, D.,

TITLE Direct Submission
JOURNAL DNA Sequencing and Technology Center,
Submitted (03-APR-2000)
Stanford University, 855 California Avenue, Palo Alto, CA 94304
USA

COMMENT On Mar 4, 2001 this sequence version replaced gi:9665085.

----- Genome Center
Center: Stanford DNA Sequencing and Technology Development

Center : DODGE DATA & ANALYTICS

Center code: SDSTDC

Web site: <http://sequence-www.stanford.edu>
Contact: hmm-info@sequence.stanford.edu

----- Project Information

Center project name: 880
Center clone name: Rp11-288018

----- Summary Statistics -----

Sequencing Vector: M13mp18; 100% of reads

sequencing vector: plasmid; plasmid_accession:
chemistry: Dye-primer; 1% of reads

Chemistry: Dye-terminator Big Dye; 99% of reads

Assembly program: Phrap; version 0.990319
Consensus quality: 190680 bases at least Q40

Consensus quality: 191287 bases at least Q30

Consensus quality: 191336 bases at least Q20
Percent N: 105549, 22409649

Insert size: 191499; sum-of-contigs

Quality coverage: 7.9x in Q20 bases; agarose-
electrophoresis: 0.1% in Q20 bases; sum-of-

* NOTE: This is a 'working draft' sequence. It currently has 8.1x coverage in 120 passes; some of the coverage is in the 1000-1200 bp range.

* consists of 3 contigs. The true order of the piece

- * is not known and their order in this sequence recorded
- * arbitrary Gaps between the contigs are represented

* runs of N , but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number

* as soon as it is available and can be preserved.

Contig	Length
12646	12646 bp
12647	12647 bp
12648	12648 bp
12649	12649 bp
12650	12650 bp
12651	12651 bp
12652	12652 bp
12653	12653 bp
12654	12654 bp
12655	12655 bp
12656	12656 bp
12657	12657 bp
12658	12658 bp
12659	12659 bp
12660	12660 bp
12661	12661 bp
12662	12662 bp
12663	12663 bp
12664	12664 bp
12665	12665 bp
12666	12666 bp
12667	12667 bp
12668	12668 bp
12669	12669 bp
12670	12670 bp
12671	12671 bp
12672	12672 bp
12673	12673 bp
12674	12674 bp
12675	12675 bp
12676	12676 bp
12677	12677 bp
12678	12678 bp
12679	12679 bp
12680	12680 bp
12681	12681 bp
12682	12682 bp
12683	12683 bp
12684	12684 bp
12685	12685 bp
12686	12686 bp
12687	12687 bp
12688	12688 bp
12689	12689 bp
12690	12690 bp
12691	12691 bp
12692	12692 bp
12693	12693 bp
12694	12694 bp
12695	12695 bp
12696	12696 bp
12697	12697 bp
12698	12698 bp
12699	12699 bp
12700	12700 bp
12701	12701 bp
12702	12702 bp
12703	12703 bp
12704	12704 bp
12705	12705 bp
12706	12706 bp
12707	12707 bp
12708	12708 bp
12709	12709 bp
12710	12710 bp
12711	12711 bp
12712	12712 bp
12713	12713 bp
12714	12714 bp
12715	12715 bp
12716	12716 bp
12717	12717 bp
12718	12718 bp
12719	12719 bp
12720	12720 bp
12721	12721 bp
12722	12722 bp
12723	12723 bp
12724	12724 bp
12725	12725 bp
12726	12726 bp
12727	12727 bp
12728	12728 bp
12729	12729 bp
12730	12730 bp
12731	12731 bp
12732	12732 bp
12733	12733 bp
12734	12734 bp
12735	12735 bp
12736	12736 bp
12737	12737 bp
12738	12738 bp
12739	12739 bp
12740	12740 bp
12741	12741 bp
12742	12742 bp
12743	12743 bp
12744	12744 bp
12745	12745 bp
12746	12746 bp
12747	12747 bp
12748	12748 bp
12749	12749 bp
12750	12750 bp
12751	12751 bp
12752	12752 bp
12753	12753 bp
12754	12754 bp
12755	12755 bp
12756	12756 bp
12757	12757 bp
12758	12758 bp
12759	12759 bp
12760	12760 bp
12761	12761 bp
12762	12762 bp
12763	12763 bp
12764	12764 bp
12765	12765 bp
12766	12766 bp
12767	12767 bp
12768	12768 bp
12769	12769 bp
12770	12770 bp
12771	12771 bp
12772	12772 bp
12773	12773 bp
12774	12774 bp
12775	12775 bp
12776	12776 bp
12777	12777 bp
12778	12778 bp
12779	12779 bp
12780	12780 bp
127	

Accession	Gene	Accession	Gene
12647	gap of unknown length	12746	gap of unknown length
12747	contig of 82215 bp in length	94961	contig of 82215 bp in length

```

* 94962 95061: gap of unknown length

```

FEATURES * 95062 191699: contig of 96638 bp in length.
Location/Qualifiers
source 1..191699
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone_1fb="RP11-288018"
/clone_1fb="RP11 human BAC library 11"
misc_feature 1..12646
/note="assembly_name:Contigs"
misc_feature 12747..94961
/note="assembly_name:Contig6"
misc_feature 95062..191699
/note="assembly_name:Contig7"
clone_end:896
clone_end:896

ORIGIN
Query Match 95.7%; Score 2000.6; DB 2; Length 191699;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 4; Indels 16; Gaps 1;
1
1 AAGAGACAGACTTATTAACCTCCAGAGTATTAAGAGCGTATGTCATGTTTATTTGTTA 60
119077 AAGAGACAGACTTATTAACCTCCAGAGTATTAAGAGCGTATGTCATGTTTATTTGTTA 119136
61 AAGAGAGTGAATAGGCTTCAAGCATGTGATATCTTCATCTTCCCGC----- 111
119137 AAGAGAGTGAATAGGCTTCAAGCATGTGATATCTTCATCTTCCCGC----- 119196
112 -----CGCTTTTGTCTTCTTCAAGTGAACCTTTTAAATGCAAGATCTAGG 164
119197 AACAACACACTTTTGTCTTCTTCAAGTGAACCTTTTAAATGCAAGATCTAGG 119256
165 CATTCAGTAACTTTTCTTCAATCAATTAAGTCAAAATGATGAAACATTTGTGCC 224
119257 CATTCAGTAACTTTTCTTCAATCAATTAAGTCAAAATGATGAAACATTTGTGCC 119316
225 TACTCTCAATCCCGGTACTCAAAATCTCTAGTGAATTAATGCTTTAAGTGAAT 284
119317 TACTCTCAATCCCGGTACTCAAAATCTCTAGTGAATTAATGCTTTAAGTGAAT 119376
285 TCAGTCCAGAGGAACTTGTGAAATTAATTTTATTTTATTTTATTTTATTTTATTTT 344
119377 TCAGTCCAGAGGAACTTGTGAAATTAATTTTATTTTATTTTATTTTATTTTATTTT 119436
345 AGCATGATTTTATTTGTTGATGTGCTGTGACACAGCCATTTCAATAGATGGA 404
119437 AGCATGATTTTATTTGTTGATGTGCTGTGACACAGCCATTTCAATAGATGGA 119496
405 GCTGTTAATTTTTCAGAAAGATTAATACATGCAAAAGTTTCAATATAAACTGGGCA 464
119497 GCTGTTAATTTTTCAGAAAGATTAATACATGCAAAAGTTTCAATATAAACTGGGCA 119556
465 TTAACAATTAATTAATACTAATAGCATCCCTTCTAGGTTTTCGCAAACTGGCTA 524
119557 TTAACAATTAATTAATACTAATAGCATCCCTTCTAGGTTTTCGCAAACTGGCTA 119616
525 TCCAAATTAATTTAGAAATGCTTGAATAAGCTAGTTATTTTCAGAGAAATGATTTTC 584
119617 TCCAAATTAATTTAGAAATGCTTGAATAAGCTAGTTATTTTCAGAGAAATGATTTTC 119676
585 ATTATTGAAGTGTCTCCCTAGCAGGCAATTTTCCTTTTCTGGAGATTAGCAAGT 644
119677 ATTATTGAAGTGTCTCCCTAGCAGGCAATTTTCCTTTTCTGGAGATTAGCAAGT 119736
645 TTGAGAGAGATGTGATGAAAGAAAGGAGAAAGGAGAGAGAGAGAGAGATTAAAA 704
119737 TTGAGAGAGATGTGATGAAAGAAAGGAGAAAGGAGAGAGAGAGAGAGATTAAAA 119796
705 GTAAGAGCTCAGACTATGAAAGTATCCCTTGTAGAAATATTTAAGAGAGCTCAGC 764

119797 GTAAGAGCTCAGACTATGAAAGTATCCCTTGTAGAAATATTTAAGAGAGCTCAGC 119856
765 TTGGTTGAAGCTGAGTTTGTGATCTTTGCAATTTTGCAGAAAGTATTTTCTGACTTGA 824
119857 TTGGTTGAAGCTGAGTTTGTGATCTTTGCAATTTTGCAGAAAGTATTTTCTGACTTGA 119916
825 ATGACAGTATGATTAATAATTTTATTTTATCTTGAAGAGCTTGTACTAGAAAAATGAA 884
119917 ATGACAGTATGATTAATAATTTTATTTTATCTTGAAGAGCTTGTACTAGAAAAATGAA 119976
885 TAAATATTGAGGTTTCTGCTGATATCTGCTGATGATGCTGCAAGAAACAGAGATTAAG 944
119977 TAAATATTGAGGTTTCTGCTGATATCTGCTGATGATGCTGCAAGAAACAGAGATTAAG 120036
945 AAATGTAATCTCCAGATCCAGATCCAGAAACCCAGAGGATGAGCAATCTATGAGATT 1004
120037 AAATGTAATCTCCAGATCCAGATCCAGAAACCCAGAGGATGAGCAATCTATGAGATT 120096
1005 TTGACATGAAATTTGGTGCATCTTGGTTATGCTGCTCACTGCTATTTAACTCTCT 1064
120097 TTGACATGAAATTTGGTGCATCTTGGTTATGCTGCTCACTGCTATTTAACTCTCT 120156
1065 GGCTTATAGCTCTTCAATCTATTAAGACAGAGCTATGCAACATCTGCTGCAAGAG 1124
120157 GGCTTATAGCTCTTCAATCTATTAAGACAGAGCTATGCAACATCTGCTGCAAGAG 120216
1125 CTCTTTAGTTAACAATTTAGAGCTAATGTTGTGTTAAACACATTTTCAACCAATAG 1184
120217 CTCTTTAGTTAACAATTTAGAGCTAATGTTGTGTTAAACACATTTTCAACCAATAG 120276
1185 TTGAGAGGAG 1244
120277 TTGAGAGGAG 120336
1245 ATCCAAATCTAAAGAGATCACTCTTCACTGAGAAAGAGCTCTGCTTGAATGGA 1304
120337 ATCCAAATCTAAAGAGATCACTCTTCACTGAGAAAGAGCTCTGCTTGAATGGA 120396
1305 AACTTACAG 1364
120397 AACTTACAG 120456
1365 TATTTATCTCACTCACTGTTTAAATATCACTTTATTTTCTAGTGAAGAACTAG 1424
120457 TATTTATCTCACTCACTGTTTAAATATCACTTTATTTTCTAGTGAAGAACTAG 120516
1425 AATTCAGCTCTTCAATTTATTAATACAGTTTAAAGCTTCTGGAAGTTTCTGTTCT 1484
120517 AATTCAGCTCTTCAATTTATTAATACAGTTTAAAGCTTCTGGAAGTTTCTGTTCT 120576
1485 CTCACCTGAGGATTTTCTCTCCCACTTGCCTTCTCTCTCTCTCTCTCTCTCTCTCT 1544
120577 CTCACCTGAGGATTTTCTCTCCCACTTGCCTTCTCTCTCTCTCTCTCTCTCTCTCT 120636
1545 TTGCAAGAGAGAAATTTTAACATTTTGGTCCAACTTCAATATGTAATTAATTAATC 1604
120637 TTGCAAGAGAGAAATTTTAACATTTTGGTCCAACTTCAATATGTAATTAATTAATC 120696
1605 ATTAAAGCAATTTAATCTTCTCTGAGAAATGCAAGGCTAAGCATAGCAAAACAA 1664
120697 ATTAAAGCAATTTAATCTTCTCTGAGAAATGCAAGGCTAAGCATAGCAAAACAA 120756
1665 AGAGAAATGCTGAGAAATTTTCCACTGAGAGCAAGCAATTTGAATTAATTTTGGCCAAA 1724
120757 AGAGAAATGCTGAGAAATTTTCCACTGAGAGCAAGCAATTTGAATTAATTTTGGCCAAA 120816
1725 GTTCTTTTATGTCATATGATGATGAGATTTGAAGAGCTATTTTATTTTATTTTATTTGCA 1784
120817 GTTCTTTTATGTCATATGATGATGAGATTTGAAGAGCTATTTTATTTTATTTTATTTGCA 120876
1785 CTAGCAATCACTCTTGGAG 1844
120877 CTAGCAATCACTCTTGGAG 120936

QY 945 AAATGTAATCTCCAAATCCAGCATCGAAACCCAGGGGTAGGCAATCTATGTAGGTT 1004
DB 156132 AAATGTAATCTCCAAATCCAGCATCGAAACCCAGGGGTAGGCAATCTATGTAGGTT 156073
QY 1005 TTGGCAATGAGTTGGTGCATCTGTGTTTATGCTGGCTCAAGCTATTAACCTCTCT 1064
DB 156072 TTGGCAATGAGTTGGTGCATCTGTGTTTATGCTGGCTCAAGCTATTAACCTCTCT 156013
QY 1065 GGCCTATAGTCTCTCATCTATTAAGACAGACGATCGAACCTTGCTGCAAGG 1124
DB 156012 GGCCTATAGTCTCTCATCTATTAAGACAGACGATCGAACCTTGCTGCAAGG 155953
QY 1125 CTCTTATGTTAATCAATTAAGCACTGCTGTTGTTTAAACACCTTTTCAACAAATAG 1184
DB 155952 CTCTTATGTTAATCAATTAAGCACTGCTGTTGTTTAAACACCTTTTCAACAAATAG 155893
QY 1185 TTCTGAGGCAAGAGAGCAATGATCTATTAAGAAAGGCTTTCCAGCATCACTTACAC 1244
DB 155892 TTCTGAGGCAAGAGAGCAATGATCTATTAAGAAAGGCTTTCCAGCATCACTTACAC 155833
QY 1245 ATCCCAAACTTAAAGATCAAATCTTCCACTGAGAAAGACTCTGCTTTGAATGGA 1304
DB 155833 ATCCCAAACTTAAAGATCAAATCTTCCACTGAGAAAGACTCTGCTTTGAATGGA 155773
QY 1305 AACTTACAGCAGAGATGACAGGCGGCAACAGCAAGCAACAAACATTGGA 1364
DB 155772 AACTTACAGCAGAGATGACAGGCGGCAACAGCAAGCAACAAACATTGGA 155713
QY 1365 TATATCTCAACTCACTGTTTAAATATATATATATATATATATATATATATATAT 1424
DB 155712 TATATCTCAACTCACTGTTTAAATATATATATATATATATATATATATATATAT 155653
QY 1425 AATGCACTCTTCAACATTAATATATATATATATATATATATATATATATATATAT 1484
DB 155652 AATGCACTCTTCAACATTAATATATATATATATATATATATATATATATATATAT 155593
QY 1485 CTCACCTGAGATATTTTTTCTCCCACTTGCCCTGTCCTGCTCTCTCTCTCTCT 1544
DB 155592 CTCACCTGAGATATTTTTTCTCCCACTTGCCCTGTCCTGCTCTCTCTCTCTCT 155533
QY 1545 TTGGCAAGGAAATTTTAAATATATATATATATATATATATATATATATATATAT 1604
DB 155532 TTGGCAAGGAAATTTTAAATATATATATATATATATATATATATATATATATAT 155473
QY 1605 ATTAAAGCATTTAATCTCTCTCTCTAGAAAAATGACAGGCTAGGCAATAGCAAAACA 1664
DB 155472 ATTAAAGCATTTAATCTCTCTCTCTAGAAAAATGACAGGCTAGGCAATAGCAAAACA 155413
QY 1665 AGAGAAATGCTAGAAATTTGGCACTGAGACAGCAATCTGAATATATATATATATAT 1724
DB 155412 AGAGAAATGCTAGAAATTTGGCACTGAGACAGCAATCTGAATATATATATATATAT 155353
QY 1725 GTCTTTTATGCTATATAGTGCAGAGATTGGAAGACTATTTTTTTTAAATGTTGCA 1784
DB 155352 GTCTTTTATGCTATATAGTGCAGAGATTGGAAGACTATTTTTTTTAAATGTTGCA 155293
QY 1785 CTAGCACTCATCTTGGAGAGACAGCCAGAGAGATGAGAGAGAGGTTTATA 1844
DB 155292 CTAGCACTCATCTTGGAGAGACAGCCAGAGAGATGAGAGAGAGGTTTATA 155233
QY 1845 AATCCATTTGAGAGATTATGCAATATTTTAAATCAAGAAAAATGTTTATATCTT 1904
DB 155232 AATCCATTTGAGAGATTATGCAATATTTTAAATCAAGAAAAATGTTTATATCTT 155173
QY 1905 TAGAATTTGATTAATACTTTATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1964
DB 155172 TAGAATTTGATTAATACTTTATGTAATGTAATGTAATGTAATGTAATGTAATGTA 155113
QY 1965 ACCAATATGATCTGTAACCAATCAACATATATATATATATATATATATATATATAC 2024
DB 155112 ACCAATATGATCTGTAACCAATCAACATATATATATATATATATATATATATAC 155053

QY 2025 AGCCAAAA 2033
DB 155052 AGCCATA 155044

RESULT 9
AX393338
LOCUS AX393338
DEFINITION Sequence 268 from Patent WO0210217.
ACCESSION AX393338
VERSION AX393338.1 GI:19701341
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
Endothelial cell expression patterns
Patent: WO 0210217-A 268 07-FEB-2002;
The Johns Hopkins University (US)
Location/Qualifiers
1. 1909
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 89.8%; Score 1878.6; DB 6; Length 1909;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 134 GACACCTTTTAAATGCAAGCACTAGGAGCAATTCAGTAATCTTGTCTTCAATCAT 193
DB 1 GACACCTTTTAAATGCAAGCACTAGGAGCAATTCAGTAATCTTGTCTTCAATCAT 60
QY 194 AAAGTCAATGTAAGAAATTTTGGCCATCTGCAATGCCGTGACGCAATTC 253
DB 61 AAAGTCAATGTAAGAAATTTTGGCCATCTGCAATGCCGTGACGCAATTC 120
QY 254 TCTAGTGAATGTAATGCTTAAAGTAATGCAATGCAAGAGAACTTGTAATTA 313
DB 121 TCTAGTGAATGTAATGCTTAAAGTAATGCAATGCAAGAGAACTTGTAATTA 180
QY 314 ATTAATTTAATTTTTTTTATCTTTCAAGCCATGATTTATTTGGTGAATGTA 373
DB 181 ATTAATTTAATTTTTTTTATCTTTCAAGCCATGATTTATTTGGTGAATGTA 240
QY 374 CTCTGACAGACCAATTTCAATAGATGAGCTGTTAATTTTCCAAAGATTAAG 433
DB 241 CTCTGACAGACCAATTTCAATAGATGAGCTGTTAATTTTCCAAAGATTAAG 300
QY 434 ACATGCAAAATTTCAATAAAACTGGGCTTTAACAATTAATTAATTAATTAAG 493
DB 301 ACATGCAAAATTTCAATAAAACTGGGCTTTAACAATTAATTAATTAATTAAG 360
QY 494 ATTCCCTTGAAGTTTGGCAACTGCGCTATCAATTAACAATTTGAAGATGTTGAA 553
DB 361 ATTCCCTTGAAGTTTGGCAACTGCGCTATCAATTAACAATTTGAAGATGTTGAA 420
QY 554 AAGCTATTAATTTTCAAGAAATGATTTCAATTAATGAACCTGTTCTCTGACGGCC 613
DB 421 AAGCTATTAATTTTCAAGAAATGATTTCAATTAATGAACCTGTTCTCTGACGGCC 480
QY 614 ATTTCCTTTTCCCTGGAGTTTGAAGATTTAGAGAGAAATAGTCAATGAAGAAAG 673
DB 481 ATTTCCTTTTCCCTGGAGTTTGAAGATTTAGAGAGAAATAGTCAATGAAGAAAG 540
QY 674 GAAAGAAAGGAGAGAGAGAGGTTTAAAGTAAAGTGTCTGACACTATGAATATCC 733
DB 541 GAAAGAAAGGAGAGAGAGAGGTTTAAAGTAAAGTGTCTGACACTATGAATATCC 600
QY 734 CTGTGTAAGAAATTTTAAAGAGGCTGAGCTTGTTGAAGCTGATTTGTATCTTCC 793

```

Db      601  CTTTGCTAGAAATATTTAAGACAGCTCAGCTTGCTGAAACCTAGTTTGTCATCTCTCC
Qy      794  ATATTGACAGAGAGATTTTCTGACTGCAATGCACTAGATGATGAAATTTTATTTAT
Db      661  ATATTGACAGAGATTTTCTGACTGCAATGCACTAGATGATGAAATTTTATTTAT
Qy      854  CATCTGAGAAAGCCTTGACTGAGAAATGAAATTAATTTAGGGTTCCTGCTCATATCT
Db      721  CATCTGAGAAAGCCTTGACTGAGAAATGAAATTAATTTAGGGTTCCTGCTCATATCT
Qy      914  GCGTTCAGTGGCCAGAAAGCAGAGAAATGAAATTAATTTAGTCTCCAGATCAGATCGA
Db      781  GCGTTCAGTGGCCAGAAAGCAGAGAAATGAAATTAATTTAGTCTCCAGATCAGATCGA
Qy      974  AACCAGAGGGGTAGGCAATTTCTATGTAGTTTGGACATGAAAGTTTGTCATCTGGTT
Db      841  AACCAGAGGGGTAGGCAATTTCTATGTAGTTTGGACATGAAAGTTTGTCATCTGGTT
Qy     1034  TATGCTGCTCACTGCTATTAACCTCTGCGCTTATGCTCTGCTCATTTATTAACA
Db      901  TATGCTGCTCACTGCTATTAACCTCTGCGCTTATGCTCTGCTCATTTATTAACA
Qy     1094  AGCAGATCGAACACTGCTCTGCGACAGAGCTCTTATGATTAACAATTTAGCAGCTACG
Db      961  AGCAGATCGAACACTGCTCTGCGACAGAGCTCTTATGATTAACAATTTAGCAGCTACG
Qy     1154  TTTGCTGTTAAACACCTTTTCAACCAATAGGTTCTGAGGCAAGAGAGCAATGACTAT
Db     1021  TTTGCTGTTAAACACCTTTTCAACCAATAGGTTCTGAGGCAAGAGAGCAATGACTAT
Qy     1214  TAAAGAAAGGCTTCCAGCATCACTTACATCCCAAACTAAAGAAATCACTCTTCC
Db     1081  TAAAGAAAGGCTTCCAGCATCACTTACATCCCAAACTAAAGAAATCACTCTTCC
Qy     1274  AACTGAGAAAGACTCTGCTGCTTGAATGAAACTTACAGAGAGAGTCAAGGCCACGG
Db     1141  AACTGAGAAAGACTCTGCTGCTTGAATGAAACTTACAGAGAGAGTCAAGGCCACGG
Qy     1334  CAACAGACAGACAAACAACAAATTTGGAATATTTATCTCACTCAGCTGTTTATATA
Db     1201  CAACAGACAGACAAACAACAAATTTGGAATATTTATCTCACTCAGCTGTTTATATA
Qy     1394  CATCTT-ATTAATTTCTAGTAGAGAACTTCAATCAAGCTCTTCAACATTTATATA
Db     1261  CATCTTATTAATTTCTAGTAGAGAACTTCAATCAAGCTCTTCAACATTTATATA
Qy     1453  GTTAAATAGCCTCTGCAAGTACTGTCTCTCACTGAGAGATTTTCTCTCCCA
Db     1321  GTTAAATAGCCTCTGCAAGTACTGTCTCTCACTGAGAGATTTTCTCTCCCA
Qy     1513  CTTGCCCCCTGTTCCCTCCCTCTCTCTCTCTTCAAGAGAAATTTTACATAAT
Db     1381  CTTGCCCCCTGTTCCCTCCCTCTCTCTCTCTTCAAGAGAAATTTTACATAAT
Qy     1573  GGGTCCAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Db     1441  GGGTCCAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Qy     1633  AAAATGACAGGCTAAGGATAGACAAACAAAGAAATGCTGAGAAATTTGCACTGG
Db     1501  AAAATGACAGGCTAAGGATAGACAAACAAAGAAATGCTGAGAAATTTGCACTGG
Qy     1693  AGACAGAGATCTGAATTAATTTTGGCAAAAGTCTTTATATGCAATATAGTCCAGA
Db     1561  AGACAGAGATCTGAATTAATTTTGGCAAAAGTCTTTATATGCAATATAGTCCAGA
Qy     1753  TTGGAAGAGATTTTATTTTATATGTCACATGCAACTCATTTGGAAGACACAGC
Db     1621  TTGGAAGAGATTTTATTTTATATGTCACATGCAACTCATTTGGAAGACACAGC
Qy     1813  CAGAGAAATGAAGTGAAGGATTAATTAATTAATTAATTAATTAATTAATTAAT

```

```

Db      1680  CAGAGAAATGAAGTGAAGGATTAATTAATTAATTAATTAATTAATTAATTAAT
Qy      1873  ATTTAATTAACAGAAATTTGCTTTATCTTTAATTTTGTATTAATTAATTAATTAAT
Db      1740  ATTTAATTAACAGAAATTTGCTTTATCTTTAATTTTGTATTAATTAATTAATTAAT
Qy      1933  CTATGACTCATGCTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Db      1800  CTATGACTCATGCTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Qy      1993  CACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Db      1860  CACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
RESULT 10
AR379796      6005 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      AR379796      Sequence 341 from patent US 6607879.
DEFINITION      AR379796
ACCESSION      AR379796
VERSION      AR379796.1      GI:40087430
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 6005)
AUTHORS      Cocke,B.G., Stuart,S.G. and Sellhame,J.J.
TITLE      Compositions for the detection of blood cell and immunological
JOURNAL      response gene expression
PATENT      US 6607879-A 341 19-AUG-2003;
FEATURES
source
1..6005
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match      88.6%;      Score 1853.4;      DB 6;      Length 6005;
Best Local Similarity 97.2%;      Pred. No. 0;
Matches 2025;      Conservative 0;      Mismatches 27;      Indels 32;      Gaps 13;
Qy      1      AAGAGACAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Db      3911  AAGAGACAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
Qy      61      AAGCAGTGAATAGCTTCAAGCATGTAATTAATTTTCACTTCCCGCC-----112
Db      3971  AAGCAGTGAATAGCTTCAAGCATGTAATTAATTTTCACTTCCCGCCNNNNNNNN
Qy      113  -----GCTTTTGTCTTCAAGTGAACCTTTTAAATGAGAACTGAG3 164
Db      4031  NNNNNNNNNNTTTTGTCTTCAAGTGAACCTTTTAAATGAGAACTGAG3 4090
Qy      165  CATTCAGTAATCTTTCCTTCAATCAATTAATTAATTAATTAATTAATTAATTAAT
Db      4091  CATTCAGTAATCTTTCCTTCAATCAATTAATTAATTAATTAATTAATTAATTAAT
Qy      225  TACTTCCATPCCCGGTGATCAATTAATCTCACTGATGATTAATTAATTAATTAAT
Db      4151  TACTTCCATPCCCGGTGATCAATTAATCTCACTGATGATTAATTAATTAATTAAT
Qy      285  TCAATGCAAGAGAACTTGGTAAATTAATTTTAA-TTTTTTTTTATCTTTAA 343
Db      4211  TCAATGCAAGAGAACTTGGTAAATTAATTTTAA-TTTTTTTTTATCTTTAA 4270
Qy      344  AAGCCATGATTTTATTTGTTGATGATGCTGATCAAGCCATTTCAATAGATG 403
Db      4271  AAGCCATGATTTTATTTGTTGATGATGCTGATCAAGCCATTTCAATAGATG 4330
Qy      404  AGCTGTTAATTAATTTTCAAGAGTATAGACATGCAAAAGTTTCAATATAAACTGGCC 463
Db      4331  AGCTGTTAATTAATTTTCAAGAGTATAGACATGCAAAAGTTTCAATATAAACTGGCC 4390
Qy      464  ATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

```

```

Db      4391 ATTAACAATAATTAATAAATAATTAACATTCCTTCTAGTCTTTTGGCCAAATGCTCT
Qy      524 ATCCATAACAATAATTTAGAAATGTTGAAAGAAAGCTAGTATATTTTCAGAGAAATGATTTT
Db      4451 ATCCATAACAATAATTTAGAAATGTTGAAAGAAAGCTAGTATATTTTCAGAGAAATGATTTT
Qy      584 CATTAATGAAGCTGTTCTCTCCAGAGAGCCATTTTCCCTTTTCTCGGAGTTTAGCAAG
Db      4511 CATTAATGAAGCTGTTCTCTCCAGAGAGCCATTTTCCCTTTTCTCGGAGTTTAGCAAG
Qy      644 TTATAGAGAGAAATGATCATGAAAGAAAGAAAGAAAGAGAGAAAGAGTTAAAG
Db      4571 TTATAGAGAGAAATGATCATGAAAGAAAGAAAGAAAGAGAGAAAGAGTTAAAG
Qy      704 AGTAAGTCTCAGACCTATGAAAGTAATCCCTTTGCTAGAAATATTTAAGACAGCTCAG
Db      4631 AGTAAGTCTCAGACCTATGAAAGTAATCCCTTTGCTAGAAATATTTAAGACAGCTCAG
Qy      764 CTGAGTTGAAGCTGAGTTTGTGATCTTCATATTTGAGAGAGAGATTTTGTGATCTGC
Db      4691 CTGAGTTGAAGCTGAGTTTGTGATCTTCATATTTGAGAGAGAGATTTTGTGATCTGC
Qy      824 AATGAGCTATGATGTAATAATTTTATTCATCTAGAAAGCTTGAATAGAAATGA
Db      4751 AATGAGCTATGATGTAATAATTTTATTCATCTAGAAAGCTTGAATAGAAATGA
Qy      884 ATTAATATTTGAGAGTTTCTCTGTCATATCTGGCTTGCATGTCGCAAGAAAGAGAAATGA
Db      4811 ATTAATATTTGAGAGTTTCTCTGTCATATCTGGCTTGCATGTCGCAAGAAAGAGAAATGA
Qy      943 GAAATATGATCTCCAAATCCAAAGCATGAAAGCCAAAGAGGCTAGGCAATTCATGTAAG
Db      4871 GAAATATGATCTCCAAATCCAAAGCATGAAAGCCAAAGAGGCTAGGCAATTCATGTAAG
Qy      1003 TTTTGGACAT-GAAGTTTGTGATCTTGTGTTATGCTGTGCTCACTGCTATTTAAACCTC
Db      4931 TTTTGGACATGAAAGTTTGTGATCTTGTGTTATGCTGTGCTCACTGCTATTTAAACCTC
Qy      1062 TCTGAGCTATGATCTCTCATCTTATTTAGCAAGACGATGAAACATTTGCTGTCACCA
Db      4991 TCTGAGCTATGATCTCTCATCTTATTTAGCAAGACGATGAAACATTTGCTGTCACCA
Qy      1122 AGGCTCTTATGTTAACAATTTAGACAGCTAATGTTTGTGTTAAACACACTTTTCA-CCAA
Db      5051 AGGCTCTTATGTTAACAATTTAGACAGCTAATGTTTGTGTTAAACACACTTTTCAACCCAA
Qy      1181 TAGGTTCTGAGCAAGCAAGAGCATGACATTTTAAAGAAAGGCTTTCCACAGCATCACTT
Db      5111 GAGGTTCTGAGCAAGCAAGAGCATGACATTTTAAAGAAAGGCTTTCCACAGCATCACTT
Qy      1241 ACAATCTCCAAATCTAAAGATCACTCTTCCAACTGA-GAAAGACCTCTGAGCTTGA
Db      5171 ACAATCTCCAAATCTAAAGATCACTCTTCCAACTGAGAAAGACCTCTGAGCTTGA
Qy      1300 ATGG---AACTTACAGCAGAGATGACAGGCAAGGCAAGCAACAAAGCAACAAAC
Db      5231 ATGGAGAAACATCTACAGCAGAGATGACAGGCAAGGCAAGCAACAAAGCAACAAAC
Qy      1357 ATTGGAAATTAATTTCTCAACTCAGCTTTTAATATACATCTTATATTTTCTAGTAGA
Db      5291 ATTGGAAATTAATTTCTCAACTCAGCTTTTAATATACATCTTATATTTTCTAGTAGA
Qy      1417 GAAACATCAAAATGAGCTCTTCAACATTTATATACAGTTTAAAGCCCTTGG-CAAGT
Db      5351 GAAACATCAAAATGAGCTCTTCAACATTTATATACAGTTTAAAGCCCTTGGCAAGT
Qy      1476 ACTTGTTCT-CTCAGCTGAGGA-TTTTCTCTCCCAAGCTTGCCTGTTCTCCCTT
Db      5411 ACTTGTTCTCCNACCTGAGGATTTTTTCTCTCCCAAGCTTGCCTGTTCTCCCTT
Qy      1534 CC--TCTTCTCCCTTGCAGAGAAATATTTAACAATTTGGGCTCAACTCATATATG

```

```

Db      5471 CCATCTGCTCCCTTGCAGAGAAATATTTAACAATTTGGGTCACACTTGAATAG
Qy      1592 TAATATTAATTAATTAAGAAAGCAATTAATCTCTTTCTAG--AAATATGACAGGCTAG
Db      5531 TAATATTAATTAATTAAGAAAGCAATTAATCTCTTTCTAGAAAGAAATGACAGGCTAG
Qy      1650 GCATAGCAAAAGCAAGAGAAATGCTGA-GAATTTGGCCATGAGAGCAAGCAATCTGAA
Db      5591 GCATAGCAAAAGCAAGAGAAATGCTGAAGAAATTTGCCATGAGCAAGCAATCTGAA
Qy      1709 TAAATATTTGCCAAAGATCTTTTATATGTCATATAGTGCAGATTTGAAGAGCTATTT
Db      5651 TAAATATTTGCCAAAGATCTTTTATATGTCATATAGTGCAGATTTGAAGAGCTATTT
Qy      1769 TTTTAAATGTTGCAATAGCAACTCATCTTCCGAAAGACACCCAGAGAAATGAAGTAG
Db      5711 TTTTAAATGTTGCAATAGCAACTCATCTTCCGAAAGACACCCAGAGAAATGAAGTAG
Qy      1829 AAGTAAAGGTTTAAATATCCATTTGTATGACATTTATCCCATATATTTTAAATCAAGAA
Db      5771 AAGTAAAGGTTTAAATATCCATTTGTATGACATTTATCCCATATATTTTAAATCAAGAA
Qy      1889 AAATGTTGTTATCTTTAGAAATTTTGTATTCATCTTATATGATCTATGATCTCATGCT
Db      5831 AAATGTTGTTATCTTTAGAAATTTTGTATTCATCTTATATGATCTATGATCTCATGCT
Qy      1949 TCTGATTAATTAAGACCAAAATATGATCTGTAACACACATCAACATATTAATTAATAA
Db      5891 TCTGATTAATTAAGACCAAAATATGATCTGTAACACACATCAACATATTAATTAATAA
Qy      2009 TATATATCTATATPAACGCCAATAAAAAAAAAAGAGAGAGAA 2052
Db      5951 TATATATCTATATPAACGCCCTCAAAAAAAAAANNNNNNNANTTAATAAA 5994

RESULT 11
AK026775 1863 bp mRNA linear PRI 12-SEP-2003
LOCUS AK026775 Homo sapiens cDNA: FLJ23122 fls, clone UMG08008.
DEFINITION AK026775
ACCESSION AK026775.1 GI:10439706
VERSION AK026775.1
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ota,T., Yamada,K., Fujii,Y., Ozaki,K., Hirono,M.,
Omoroi,Y., Ota,T., Suzuki,Y., Odayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
unpublished
TITLE NEDO human cDNA sequencing project
JOURNAL 2 (bases 1 to 1863)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Odayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
DIRECT SUBMISSION Direct Submission
JOURNAL Submitted (29-NOV-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source location/Qualifiers
1..1863
/organism="Homo sapiens"

```

/mol_type="mrna"
/db_xref="taxon:9606"
/clone="LN308008"
/issue_type="human lung"
/clone_lib="LNG"
/note="Cloning vector pME18SFL3"

Query Match 88.3%; Score 1845.6; DB 9; Length 1863;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1859; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

178 TTGCTTCAATCAATTAAGTCAATGTATGAAAACATTTTGTGCTTACTCTCATACC 237
1 TTGCTTCAATCAATTAAGTCAATGTATGAAAACATTTTGTGCTTACTCTCATACC 60
238 CCGTGTACTCAATCTCTACTGTATGAAATATGCTTAAAGTAAATCAAGTCCAAAGA 297
61 CTGTGTACTCAATCTCTACTGTATGAAATATGCTTAAAGTAAATCAAGTCCAAAGA 120
298 GAAGTGTGTGAATAATTAATTTTATTTTATCTTTTACCAAGCCATGATTTT 357
121 GAAGTGTGTGAATAATTAATTTTATTTTATCTTTTACCAAGCCATGATTTT 180
358 ATTGCTGTATGTGTGCTGTATGCAAGCCATTTCAATAGATGAGAGCTGTATTT 417
181 ATTGCTGTATGTGTGCTGTATGCAAGCCATTTCAATAGATGAGAGCTGTATTT 240
418 TTCCAAAGATATAGACATGCAAAAAGTTCAATATAAACTGGCCATTAACAAATAAT 477
241 TTCCAAAGATATAGACATGCAAAAAGTTCAATATAAACTGGCCATTAACAAATAAT 300
478 TAATAAATTAATTAATTAATTTTATTTTATCTTTTACCAAGCCATGATTTT 537
301 TAATAAATTAATTAATTAATTTTATTTTATCTTTTACCAAGCCATGATTTT 360
538 TTGAGATCGTGAATAAGTATTAATTTTATGAGAAATGATTTTATTTGAAGTGTG 597
361 TTGAGATCGTGAATAAGTATTAATTTTATGAGAAATGATTTTATTTGAAGTGTG 420
598 TTCTCCCTAGACAGCCATTTTCTTTTCTGAGAGTTTATGCAAGTTTATGAGAGATA 657
421 TTCTCCCTAGACAGCCATTTTCTTTTCTGAGAGTTTATGCAAGTTTATGAGAGATA 480
658 GTGATGAAAAGAAAGGAGAAAGGAGAGAGAGGTTAAAGATAGTGTGCA 717
481 GTGATGAAAAGAAAGGAGAAAGGAGAGAGAGGTTAAAGATAGTGTGCA 540
718 CCTATGACGTATCCCTTTGCTAGAAATATTTAAGACAGCTCAGCTGTGTAAGTGTG 777
541 CCTATGACGTATCCCTTTGCTAGAAATATTTAAGACAGCTCAGCTGTGTAAGTGTG 600
778 AGTTTGTATCTTCCATATTTGCAAGAGATTTTCTGACTTGCATGAGCTAAGT 837
601 AGTTTGTATCTTCCATATTTGCAAGAGATTTTCTGACTTGCATGAGCTAAGT 660
838 TAAATTTTATTTATCATCTAGAAAGCTTGACATAGAAAATGATTAATATGAGG 897
661 TAAATTTTATTTATCATCTAGAAAGCTTGACATAGAAAATGATTAATATGAGG 720
898 TTTCCTGTCTATCTGCTGTGATGTCAGAAAGAGAGATAGAAATATATCTCC 957
721 TTTCCTGTCTATCTGCTGTGATGTCAGAAAGAGAGATAGAAATATATCTCC 780
958 AACATCAAGCATCGAAACCAAGAGGATGAGCAATCTATGAGTTTGAAGTGAAGT 1017
781 AACATCAAGCATCGAAACCAAGAGGATGAGCAATCTATGAGTTTGAAGTGAAGT 840
1018 TTGCTGTATCTGCTGTGATGTCAGAAAGCTGTATTAAGCTCTGCTGTATATGCTC 1077
841 TTGCTGTATCTGCTGTGATGTCAGAAAGCTGTATTAAGCTCTGCTGTATATGCTC 900
1078 TTGCTGTATCTGCTGTGATGTCAGAAAGCTGTGCTGTGCAAGAGCTCTTATGTAAC 1137

901 TTGCTGTATCTGCTGTGATGTCAGAAAGCTGTATTAAGCTCTTATGTAAC 960
1138 AATTGACAGCTACTGTGTTGTGTTAAACACACTTTTACCAATATAGTTCTGAGCAAC 1197
961 AATTGACAGCTACTGTGTTGTGTTAAACACACTTTTACCAATATAGTTCTGAGCAAC 1020
1198 GAGAGCAATGACTATTTAAAGAAAGCTTTCCAGATGACTTACATCCCAAACTAA 1257
1021 GAGAGCAATGACTATTTAAAGAAAGCTTTCCAGATGACTTACATCCCAAACTAA 1080
1258 AAGATTAAGCTCTTCCAGCTGAGAAAGACTCTGCTGTGATGAGAACTTACAGAGA 1317
1081 AAGATTAAGCTCTTCCAGCTGAGAAAGACTCTGCTGTGATGAGAACTTACAGAGA 1140
1318 GAGTCAAGGCAAGGCAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1377
1141 GAGTCAAGGCAAGGCAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1200
1378 TCACTTTTAAATATATATCTTATTTATTTTCTGATGAGAACTTACAAATCAGCTCTT 1437
1201 TCACTTTTAAATATATATCTTATTTATTTTCTGATGAGAACTTACAAATCAGCTCTT 1260
1438 CAACATTTATATACAGTTTATATAGCTCTTGAAGTACTGTTCTGACCTGAGATA 1497
1261 CAACATTTATATACAGTTTATATAGCTCTTGAAGTACTGTTCTGACCTGAGATA 1320
1498 TTTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1557
1321 TTTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1558 ATATTTAATATATTTGAGTCAACTTCAATATATATATATATATATATATATATAT 1617
1381 ATATTTAATATATTTGAGTCAACTTCAATATATATATATATATATATATATATAT 1440
1618 AACTTCTTTCTGAAAAATGCAAGGCTAAGCATGACAAACAAAGAAATGCTGA 1677
1441 AACTTCTTTCTGAAAAATGCAAGGCTAAGCATGACAAACAAAGAAATGCTGA 1500
1678 GAAATTTGCCAGTGGAGACAGCAATCTGAATATATTTGCAAAAGTCTTTATATG 1737
1501 GAAATTTGCCAGTGGAGACAGCAATCTGAATATATTTGCAAAAGTCTTTATATG 1560
1738 CATATAGTGTGAGATTTGAGAGATTTTATTTTATGTTGCAATAGCAATCATC 1797
1561 CATATAGTGTGAGATTTGAGAGATTTTATTTTATGTTGCAATAGCAATCATC 1619
1798 TTGGAAGACACAGCCAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1857
1620 TTGGAAGACACAGCCAGAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1679
1858 GCATTTATCCCATATATTTTAAATTCAGAAAAATGTTGTTATCTTATAGAAATTTGAT 1917
1680 GCATTTATCCCATATATTTTAAATTCAGAAAAATGTTGTTATCTTATAGAAATTTGAT 1739
1918 TCAATTTATTTATGACTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1977
1740 TCAATTTATTTATGACTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1799
1978 CTGTAAACCAATGACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2037
1800 CTGTAAACCAATGACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1859
2038 AAAA 2041
1860 AAAA 1863

RESULT 12
BC029357 1490 bp mRNA linear PRI 19-NOV-2003
LOCUS Homo sapiens cDNA clone MGC:32530 IMAGE:433776, complete cds.
DEFINITION
ACCESSION BC029357

VERSION BC029357.1 GI:20810417
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1490)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.M., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedl, T.B., Toshitsuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.O., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzinski, M.I., Skalka, J., Smalls, D.E., Scherzer, A., Schein, J.E., Jones, S.J. and Marra, M.A. 2002. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1490)
Strausberg, R.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
TITLE NIH-MGC Project URL: <http://mgc.nci.nih.gov>
REMARK COMMENT
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdepaxl@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAP Plate: 41 Row: d Column: 6.
Location/Qualifiers
1. 1490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:32530 IMAGE:433776"
/tissue_type="Skeletal Muscle"
/clone_id="NIH_MGC_81"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
415. 666
/codon_start=1
/product="Unknown (protein for MGC:32530)"
/protein_id="AAH29357.1"
/db_xref="GI:20810418"
/translation="MTGNILCPHLHPCTQILYCNMYALSRIQCGCEGLSEIVRPFPP
ILYKMDPIWLCALYTSHPNRELLIIIFORVIDWQKFG"

Best Local Similarity 98.0%; Pred. No. 2e-224;
Matches 1257; Conservative 0; Mismatches 9; Indels 16; Gaps 1;
QY 1 AAGAGACAGCTATTAATCCACAGTTAATTAAGACGATGTCATGTTATTTGTTA 60
DB 198 AAGAGACAGCTATTAATCCACAGTTAATTAAGACGATGTCATGTTATTTGTTA 257
QY 61 AAGCAGTGTGAATAGCCTTCAGACATGTAATATCTTCATCTTCCCGC----- 111
DB 258 AAGCAGTGTGAATAGCCTTCAGACATGTAATATCTTCATCTTCCCGCACAATAC 317
QY 112 -----CGTTTTTCTTTCTTCAAGTGAACACCTTTAAATGACAACTACTAGAG 164
DB 318 ACAACACACTTTTCTTTCTTCAAGTGAACACCTTTAAATGACAACTACTAGAG 377
QY 165 CATTGACATCTTCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 224
DB 378 CATTGACATCTTCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 437
QY 225 TACTTCCATACCCCGTGTACTCAATTCCTACTGTATGAATTAAGCTTAGTAGAAT 284
DB 438 TACTTCCATACCCCGTGTACTCAATTCCTACTGTATGAATTAAGCTTAGTAGAAT 497
QY 285 TCACTGCAAGAGAACTTGTGAATTAATTTAATTTTATTCCTTTACAA 344
DB 498 TCACTGCAAGAGAACTTGTGAATTAATTTAATTTTATTCCTTTACAA 557
QY 345 AGCAGTGAATTTATTTGTTGTTATGTCGTGTACACAGCATTTCAATGATGGA 404
DB 558 AGCAGTGAATTTATTTGTTGTTATGTCGTGTACACAGCATTTCAATGATGGA 617
QY 405 GCTGTATATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGAT 464
DB 618 GCTGTATATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGAT 677
QY 465 TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
DB 678 TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
QY 525 TCCATATCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
DB 738 TCCATATCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 585 ATTAATGAATCTGTCCTCCAGAGCCATTTCCCTTTCTGAGAGTTAGCAAGT 644
DB 798 ATTAATGAATCTGTCCTCCAGAGCCATTTCCCTTTCTGAGAGTTAGCAAGT 857
QY 645 TTAGAGAGAAATGTCATGAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
DB 858 TTAGAGAGAAATGTCATGAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 917
QY 705 GTAAGTCAGACCTATGAAGATATCCCTTGTGAATTAATTAAGACAGCTCAGC 764
DB 918 GTAAGTCAGACCTATGAAGATATCCCTTGTGAATTAATTAAGACAGCTCAGC 977
QY 765 TTGCTGAATAGTGTGTTGTCATCTTCATTTTGAAGAGAGATTTCTGACTGCA 824
DB 978 TTGCTGAATAGTGTGTTGTCATCTTCATTTTGAAGAGAGATTTCTGACTGCA 1037
QY 825 ATGACGCTAGATGAATTAATTTATTTATCATCTAGAAAAGCTTGAATGAATGAA 884
DB 1038 ATGACGCTAGATGAATTAATTTATTTATCATCTAGAAAAGCTTGAATGAATGAA 1097
QY 885 TAAATATTGAGAGTTTCTGTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
DB 1098 TAAATATTGAGAGTTTCTGTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1157
QY 945 AAATGTAATCCCAACATCCAGACATGAACCAAGAGAGAGAGAGAGAGAGAGAG 1004
DB 1158 AAATGTAATCCCAACATCCAGACATGAACCAAGAGAGAGAGAGAGAGAGAG 1217
QY 1005 TTGACATGAAGTTGTCATCTTGGTTATGCTGCTCAATGCTATTAACCTCTCT 1064

Db 1218 TTGACATGAAAGTTGGTCATCTTGGTTATGCTGGGTCACTGCTATTAACTCTCT 1277
QY 1065 GGGTTATAGTCTTTCATCTTATTAAGACAGCAGTATCGAACCTTGTTCGACAGG 1124
Db 1278 GGGTTATAGTCTTTCATCTTATTAAGACAGCAGTATCGAACCTTGTTCGACAGG 1337
QY 1125 CTCTTATTAAGACATTTAGAGAGCTGTTGTGTTAAACACACTTTCACCAATAGG 1184
Db 1338 CTCTTATTAAGACATTTAGAGAGCTGTTGTGTTAAACACACTTTCACCAATAGG 1397
QY 1185 TTCTAGGCAACGAGACCAATGACTATTAAAGAAAGCTTCCAGCATCTTAAC 1244
Db 1398 TTCTAGGCAACGAGACCAATGACTATTAAAGAAAGCTTCCAGCATCTTAAC 1457
QY 1245 ATCCCAAACTTAAAGATCA 1266
Db 1458 ATCCCAAACTTAAAGATCA 1479

RESULT 13
HSM802503 1121 bp mRNA linear PRI 18-FEB-2000
LOCUS Homo sapiens mRNA; CDNA DKFZ58611524 (from clone DKFZ58611524).
DEFINITION AL157502
ACCESSION AL157502.1 GI:7018552
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1121)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (15-FEB-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZ58611524) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://www.mips.biochem.mpg.de/proj/CDNA/>.
Location/Qualifiers
source 1..1121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ58611524"
/issue_type="uterus"
/clone_1ib="586 (synonym: hute1). Vector pSPORT1; host
DH10B; sites NotI + SalI/MuI"
/dev_stage="adult"
1068..1073
polya_signal
polya_site
1093

ORIGIN
Query Match 53.2%; Score 1112; DB 9; Length 1121;
Best Local Similarity 99.6%; Pred. No. 1.1e-202;
Matches 1115; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 936 GAGATAGAAATGTATCTCCACATCCAGATCGAAGCCAGGGGTAGCAATCT 995
Db 1 GAGAAATGAAAGATGATCTCCACATCCAGATCGAAGCCAGGGGTAGCAATCT 60
QY 996 ATGTAGTTTGGACATGAGTTGGTGCATCTTGTATGCTGGCTCACTGCTATTA 1055
Db 61 ATGTAGTTTGGACATGAGTTGGTGCATCTTGTATGCTGGCTCACTGCTATTA 120
QY 1056 AACCTCTGGCTTATAGTCTTTCATCTTATTAAGACAGCAGTATCGAATCTGCT 1115
Db 121 AACCTCTGGCTTATAGTCTTTCATCTTATTAAGACAGCAGTATCGAATCTGCT 180

QY 1116 CGACAAAGGCTCTTATGTAACATTTAGACACTAGCTGTTGTGTTAAACACACTTTCA 1175
Db 181 CGACAAAGGCTCTTATGTAACATTTAGACACTAGCTGTTGTGTTAAACACACTTTCA 240
QY 1176 CCAATATAGGTTCTGAGGCAACGAGAGCAATGACTATTAAAGAAAGGCTTCCAGCAT 1235
Db 241 CCAATATAGGTTCTGAGGCAACGAGAGCAATGACTATTAAAGAAAGGCTTCCAGCAT 300
QY 1236 CACTTACATCCCAAACTTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCT 1295
Db 301 CACTTACATCCCAAACTTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCT 360
QY 1296 TTGAATGAAACTTACAGAGAGTCAAGGCCAGGCAACAGCAACACAAACAA 1355
Db 361 TTGAATGAAACTTACAGAGAGTCAAGGCCAGGCAACAGCAACACAAACAA 420
QY 1356 CATTTGAATATTTATCTCACTCAGCTTTTAAATAATATCTTATTTTCTAGTAG 1415
Db 421 CATTTGAATATTTATCTCACTCAGCTTTTAAATAATATCTTATTTTCTAGTAG 480
QY 1416 AGAACTCAAAATCAGCTCTTCAACATTTATATAGTTTAAAGCCTCTTGAAGTT 1475
Db 481 AGAACTCAAAATCAGCTCTTCAACATTTATATAGTTTAAAGCCTCTTGAAGTT 540
QY 1476 ACTTGTCTCTCACTGAGGATTTTTTCTCTCCCACTTGGCCCTGTCTCCCTCC 1535
Db 541 ACTTGTCTCTCACTGAGGATTTTTTCTCTCCCACTTGGCCCTGTCTCCCTCC 600
QY 1536 TCTTCCCTCTTCAAGAGAAATTTTAAATATTTGAGTCCCACTGAATATGAT 1595
Db 601 TCTTCCCTCTTCAAGAGAAATTTTAAATATTTGAGTCCCACTGAATATGAT 660
QY 1596 AATTAATACATTAAGACATTTACTCTCTTCAAGAAATGCAAGGCTTAAGCATAG 1655
Db 661 AATTAATACATTAAGACATTTACTCTCTTCAAGAAATGCAAGGCTTAAGCATAG 720
QY 1656 ACAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGCAATGAAATAT 1715
Db 721 ACAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACAAAGCAATGAAATAT 780
QY 1716 TTGCCAAAGTTCTTTTATAGTCATATAGTGCAGATTTGAAGAGCTATTTTTTT 1775
Db 781 TTGCCAAAGTTCTTTTATAGTCATATAGTGCAGATTTGAAGAGCTATTTTTTT 840
QY 1776 ATGTGCAATACCACTCATCTTCCGAGAGACACACCGAGAGAAAGATAGAGTGA 1835
Db 841 ATGTGCAATACCACTCATCTTCCGAGAGACACACCGAGAGAAAGATAGAGTGA 900
QY 1836 AGTTTAAATCATTTGTAGCATTTATCCCATATTTTAAATTCAGAAAAATTTG 1895
Db 901 AGTTTAAATCATTTGTAGCATTTATCCCATATTTTAAATTCAGAAAAATTTG 960
QY 1896 GTTATCTTAAAGATTTGTATTCATATCTTATGACATGACATGACCTCTGGAT 1955
Db 961 GTTATCTTAAAGATTTGTATTCATATCTTATGACATGACATGACCTCTGGAT 1020
QY 1956 AAATTAAGCAACAAATGATCTGPAACACATATCAATATATTTATTTAAATATAT 2015
Db 1021 AAATTAAGCAACAAATGATCTGPAACACATATCAATATATTTATTTAAATATAT 1080
QY 2016 CTATATTAAGCCCAAAAGAAAAAGAGAGAGAGAAAA 2055
Db 1081 CTATATTAAGCCCAAAAGAAAAAGAGAGAGAGAAAA 1120

RESULT 14
AX330124/c 331 bp DNA linear PAT 09-JAN-2002
LOCUS AX330124
DEFINITION Sequence 633 from Patent WO0194629.
ACCESSION AX330124
VERSION AX330124.1 GI:18103102
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Euteria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
Horrigan, S., Soppet, D.R., and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 633 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES 1. .331
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 15.8%; Score 331; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 3.5e-53;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1698 AGCAATCTGAATTAATTAATTTGCCAAAGTCTTTTATGTCATATAGTGCAGATTGA 1757
DB 331 AGCAATCTGAATTAATTAATTTGCCAAAGTCTTTTATGTCATATAGTGCAGATTGA 272
QY 1758 AGGAGCTATTTTTTTTAAATGTTGCACTGACACTCATCTTCGGAAGACACAGCCAGGA 1817
DB 271 AGGAGCTATTTTTTTTAAATGTTGCACTGACACTCATCTTCGGAAGACACAGCCAGGA 212
QY 1818 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCACTTATCCCATATATTT 1877
DB 211 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCACTTATCCCATATATTT 152
QY 1878 AAATTCAGAAAAAATGTTGTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 1937
DB 151 AAATTCAGAAAAAATGTTGTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 92
QY 1938 TGACTCATGCTTCTGATTAATTAAGCAACCAATATGATCTGTAACCAATCAGCAT 1997
DB 91 TGACTCATGCTTCTGATTAATTAAGCAACCAATATGATCTGTAACCAATCAGCAT 32
QY 1998 ATTATATTAATTAATTAATCTATATTAACAGCC 2028
DB 31 ATTATATTAATTAATTAATCTATATTAACAGCC 1
RESULT 15
AX334654/C 331 bp DNA linear PAT 09-JAN-2002
LOCUS AX334654
DEFINITION Sequence 5163 from Patent WO0194629.
ACCESSION AX334654
VERSION AX334654.1 GI:18125373
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Euteria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
Horrigan, S., Soppet, D.R., and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 5163 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES 1. .331
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 15.8%; Score 331; DB 6; Length 331;

Best Local Similarity 100.0%; Pred. No. 3.5e-53;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1698 AGCAATCTGAATTAATTAATTTGCCAAAGTCTTTTATGTCATATAGTGCAGATTGA 1757
DB 331 AGCAATCTGAATTAATTAATTTGCCAAAGTCTTTTATGTCATATAGTGCAGATTGA 272
QY 1758 AGGAGCTATTTTTTTTAAATGTTGCACTGACACTCATCTTCGGAAGACACAGCCAGGA 1817
DB 271 AGGAGCTATTTTTTTTAAATGTTGCACTGACACTCATCTTCGGAAGACACAGCCAGGA 212
QY 1818 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCACTTATCCCATATATTT 1877
DB 211 GAATGAAGTGAAGTGAAGTGAATTAATTCATTGTAAGCACTTATCCCATATATTT 152
QY 1878 AAATTCAGAAAAAATGTTGTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 1937
DB 151 AAATTCAGAAAAAATGTTGTTATCTTTAGAAATTTGTATCAATCTTATGTAATG 92
QY 1938 TGACTCATGCTTCTGATTAATTAAGCAACCAATATGATCTGTAACCAATCAGCAT 1997
DB 91 TGACTCATGCTTCTGATTAATTAAGCAACCAATATGATCTGTAACCAATCAGCAT 32
QY 1998 ATTATATTAATTAATTAATCTATATTAACAGCC 2028
DB 31 ATTATATTAATTAATTAATCTATATTAACAGCC 1
Search completed: May 5, 2004, 16:28:42
Job time : 8128 secs